

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

## STAFF USE ONLY

## Type of Search

## Vendors and cost where applicable

Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr. Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 19:01:33 ; Search time 1433.84 Seconds

(without alignments)  
1739.357 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405  
1 atgggttgtaactgtatcat.....ccctgtcacgcgtctcctca 405

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba1: \*  
2: gb\_ba2: \*  
3: gb\_ba3: \*  
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95: em\_pi: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	289.6	71.5	805	56	AF238196
2	272.2	67.2	446	10	108288
3	272.2	67.2	462	95	S78361
4	251.4	62.1	405	92	HSIGHX11
5	248.2	61.3	433	9	AR024343
6	248.2	61.3	433	9	AR045196
7	245	60.5	405	10	131950
8	245	60.5	405	10	178562
9	245	60.5	405	10	178617
10	245	60.5	405	92	HSBUD114H
11	245	60.5	405	94	MUSIGHM195
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12 243.4 60.1 405 10 E16346 E16346 DNA encoding
13 243.4 59.1 1773 10 E14571 E14571 Mouse mRNA
14 241.3 59.7 414 88 AF062257 AF062257 Homo sapi
15 241.3 59.7 451 94 M27821 M27821 Mouse anti-
16 241.3 59.7 471 94 M27821 M27821 Mouse anti-
17 241.2 59.6 700 94 M27821 M27821 Mouse Ig ac
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19 240.2 59.3 402 93 M28251 M28251 Mouse Ig re
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23 239 59.0 418 10 M28251 M28251 Mouse Ig re
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37 237.4 58.6 418 10 E16326 E16326 DNA coding
38 237.4 58.6 418 10 E16326 E16326 DNA coding
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## ALIGNMENTS

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RESULT 1
LOCUS AF239196 805 bp mRNA SYN 03-JUL-2000
DEFINITION Synthetic construct BCL1 lymphoma-derived single chain idotype
VERSION AF239196
KEYWORDS AF239196.1 GI:8925314
SOURCE Synthetic construct.
ORGANISM Artificial sequence.
REFERENCE 1 (bases 1 to 805)
AUTHORS Kersten,M.W.J., van den Berk,P.C.M., van Oers,M.H.J. and
Kersten,M.W.J.
TITLE Murine BCL1 lymphoma-derived single chain antibody (scfv) sequence
REFERENCE 2 (bases 1 to 805)
AUTHORS Schreurs,M.W.J., van den Berk,P.C.M., van Oers,M.H.J. and
Kersten,M.W.J.
TITLE Direct Submission
JOURNAL Submitted (24-FEB-2000) Immunology, The Netherlands Cancer
Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands
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1. 805
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Best local Similarity 83.6%; Pred No 2.1e-80;
Matches 341; Conservative 0; Mismatches 64; Indels 3; Gaps 1;
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QY 121 tgcacagctccgcgtacacattcaccgattatctctacagtggtgaacagctcc 180
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QY 181 ggcacagctccgcgtacacattcaccgattatctctacagtggtgaacagctcc 240
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LOCUS 108288 446 bp PAT 02-DEC-1994
DEFINITION Sequence 4 from Patent EP 0380068.
VERSION 108288
KEYWORDS 108288.1 GI:589000
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 446)
AUTHORS Zerler,B.D.
TITLE An expression system for production of chimeric monoclonal
antibodies
JOURNAL Patent: EP 0380068-A1 4 01-AUG-1990;
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BASE COUNT 117 a 110 c 113 g 106 t
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367. 405
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Best Local Similarity 76.3%; Pred. No. 2.2e-68;
Matches 309; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 1 atgggttggaactgtatcatctctctctctgtgttaccaagctacaggtgtgactccag 60
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QY 361 tataagactactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 405
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Db 361 TATATGCACTACTGGGGCAGGAACCTGTGTACACGCTCTCTCA 405
RESULT 5
AR024343 433 bp DNA PAT 05-DEC-1998
LOCUS Sequence 111 from patent US 5795965.
DEFINITION AR024343
ACCESSION AR024343
VERSION AR024343.1 GI:3977637
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 433)
AUTHORS Tsuchiya,M., Sato,K., Bendig,M.Margaret, Jones,S.Tarran and
Saidanha,J.William.
TITLE Reshaped human to human interleukin-6 receptor
JOURNAL Patent: US 5795965-A 111 18-AUG-1998;
FEATURES
source 1. 433
location/Qualifiers
BASE COUNT 94 a 108 c 128 g 103 t
ORIGIN
Query Match 61.3% Score 248.2; DB 9; Length 433;
Best Local Similarity 75.8%; Pred. No. 2.2e-67;
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RESULT 6
AR045196 433 bp DNA PAT 29-SEP-1999
LOCUS Sequence 111 from patent US 5817790.
DEFINITION AR045196
ACCESSION AR045196
VERSION AR045196.1 GI:5966661
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 433)
AUTHORS Tsuchiya,M., Sato,K., Bendig,M.Margaret, Jones,S.Tarran and
Saidanha,J.William.
TITLE Reshaped human antibody to human interleukin-6 receptor
JOURNAL Patent: US 5817790-A 111 06-OCT-1998;
FEATURES
source 1. 433
location/Qualifiers
BASE COUNT 94 a 108 c 128 g 103 t
ORIGIN
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## RESULT 12

E16346

LOCUS 405 bp DNA PAT 28-JUL-1999  
DEFINITION DNA encoding immunoglobulin VH region of anti-human Fas mouse  
monoclonal antibody CH11.

E16346

ACCESSION E16346.1 GI:5711029

VERSION

KEYWORDS JP 1998165178-A/9.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 405)  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Shibata, M. and Watanabe, Y.  
DNA ENCODING VARIABLE REGION OF ANTI-FAS ANTIBODY AND ANTI-FAS  
Patent: JP 1998165178-A 9 23-JUN-1998;  
IGAKU SEIBUTSUGAKU KENKYUSHO:KK  
OS Mus sp. (mouse)  
PN JP 1998165178-A/9  
PD 23-JUN-1998  
PF 01-JUL-1997 JP 1997191769  
PR 02-JUL-1996 JP 96P 172228, 09-OCT-1996 JP 96P 268737 PI  
SHIBATA MASAO, WATANABE YUKO

PC C12N15/00,C07K16/18,C12P21/02,(C12P21/02,C12R1:91); CC  
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CC topology: Linear;  
FH key location/Qualifiers  
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FT /organism="Mus sp."  
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FT sig\_peptide 1..57  
FT V\_region 58..405.  
FEATURES  
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BASE COUNT 103 a 102 c 102 g 98 t  
ORIGIN

Query Match 60.1%; Score 243.4; DB 10; Length 405;  
Best Local Similarity 75.1%; Pred. No. 7.2e-66;

Matches 304; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

OY 1 atgggttggaactgtatcatctctctctgtgtaccacagctacaggtgtgactccag 60  
DB 1 ATGGGATGGAGCTGGATCTTCTCTCCCTGTCAGGAACGACGGCTCCACTCTGAG 60  
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OY 361 tatatgactactgggtgtcaaggtacacctgtcacccgtctctca 405  
DB 361 GCTATGACTACTGGGTCACAGAACCTCAGTCACGCTCTCTCA 405

## RESULT 13

E14571

LOCUS 1773 bp DNA PAT 28-JUL-1999  
DEFINITION Mouse mRNA for immunoglobulin heavy chain of anti-human Fas mouse  
monoclonal antibody CH11.

E14571

ACCESSION E14571.1 GI:5709254

VERSION

KEYWORDS JP 1997322796-A/1.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

1 (bases 1 to 1773)  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Serizawa, N., Nakahara, K., Ichikawa, K. and Yonehara, S.  
DNA CODING VARIABLE REGION OF MONOCLONAL ANTIBODY, AND RECOMBINED  
ANTIBODY  
Patent: JP 1997322796-A 1 16-DEC-1997;  
SANKYO CO LTD  
OS Mus musculus (mouse)  
PN JP 1997322796-A/1  
PD 16-DEC-1997

PF 28-MAR-1997 JP 1997076890  
PI 01-APR-1996 JP 96P 78570  
PR SERIZAWA NOBUKI, NAKAHARA KAORI, ICHIKAWA KIMIHISA, PI  
YONEHARA SHIN  
PC C12P21/08.C07H21/04.C07K16/28.C12N1/21.C12N15/09, PC  
C12P21/02/A61K39/395,  
PC A61K39/395.G01N33/531.G01N33/577,(C12P21/08.C12R1:19), PC  
(C12N1/21.C12R1:19),  
PC (C12P21/02.C12R1:19);  
CC strandedness: Double;  
CC topology: Linear;  
FH key Location/Qualifiers  
FH source 1..1773  
FT /organism='Mus musculus'  
FT /cell\_type='hybridoma'  
FT /cell\_line='CH11'  
FT CDS 1..1773  
FT /product='immunoglobulin heavy chain of  
FT sig\_peptide 1..57  
FT V\_region 58..405  
FT misc\_feature 406..1770  
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Best Local Similarity 75.1%; Pred. No. 8.9e-66;  
Matches 304; Conservative 0; Mismatches 101; Indels 0; Gaps 0;  
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DB 1 ATGGGATGGAGCTGGATCTTCTTCCTGCTGTCAGAGAACTGACGGCGTCTGAG 60  
QY 61 gtccagctgtgctgagctgtgaggtggaagaagcctggagcctcagatgaagtgtcc 120  
DB 61 GTCCAGCTTGCAGAGCTGAGAGCTGAGCTGGAACCTGGGCGCTGAGATGATCC 120  
QY 121 tgcgaagcttcgcgtacacatctactgattatgctatcagatggtgagcaggtccct 180  
DB 121 TGCAGGCTTCTGATACACATTCTACTGACTACACATGCTGCTGAGAGACCAT 180  
QY 181 ggcacagggcctcagctgagatltggaatttaataattactatgataatacaactaac 240  
DB 181 GGAAGAGCCTTGATGATGATATTTATCTTACAAATGGTGCTGCTGCTCAAC 240  
QY 241 cagaagatttaagggcagaagccacaatgactgtagacaagtcgacagcactatag 300  
DB 241 CAGAAGTTTCAAGGACAGGACCATTTGACAAATTTCTCCGACAGCCTCATG 300  
QY 301 gaacttagtcttctgagatctgagatagcagcgtttattactgtgcaagaagcgtctg 360  
DB 301 GAGCTCCGACGCTGACATCTGAGACTCTGCTGCTTATTACTGTGCAAGAGTACTAT 360  
QY 361 tataatggaactactggtggtcaaggtaacctgttcaacctctca 405  
DB 361 GCTATGAGACTACTGGGGTCAAGAGACCTCAGTACCGCTCCCA 405

RESULT 14  
AF062257 414 bp mRNA PRI 02-JUN-1998  
LOCUS Homo sapiens clone Xu-12 immunoglobulin heavy chain variable region  
DEFINITION (IGH) mRNA, partial cds.  
ACCESSION AF062257  
VERSION AF062257.1 GI:3170980

KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Wang, X. and Stollar, B.D.  
TITLE Autoactivity and immunoglobulin VH gene expression in aging humans  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 414)  
AUTHORS Wang, X. and Stollar, B.D.  
TITLE Direct Submission  
JOURNAL Submitted (24-APR-1998) Biochemistry Department, Tufts University  
School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA  
FEATURES  
source Location/Qualifiers  
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Best Local Similarity 76.2%; Pred. No. 2.3e-65;  
Matches 313; Conservative 0; Mismatches 92; Indels 6; Gaps 1;  
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DB 181 GGACAGGCGCTTGATGATGATGATGATCAACCTTACAGTGGTGGCAAAACTATGCA 240  
QY 241 cagaagatttaagggcagaagccacaatgactgtagacaagtcgacagcactatag 300  
DB 241 CAGAAGTTTCAAGGAGGCTCACCATGACAGGACAGCTCATCAGACGCTCATATG 300  
QY 301 gaacttagtcttctgagatctgagatagcagcgtttattactgtgcaagaagcgtctg 359  
DB 301 GAGCTGAGCAGGCTGAGATCTGACACACGCGCGTGTATTACTGTGCGAGAGACGCCGA 360  
QY 360 -----gtataatggaactactggtggtcaaggtaacctgttcaacctctca 405







GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 18:58:13 ; Search time 1635.84 Seconds  
(without alignments)  
36.187 Million cell updates/sec

Title: US-09-249-011-5  
Perfect score: 405  
Sequence: 1 atgggttggaactgtatcat.....ccctgtcacgcgtcctcta 405

Scoring table: IDENTITY\_NMC  
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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 234: gb\_gss34:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	233.8	57.7	771	144	BF140551	BF140551 601787584
2	232	57.3	724	144	BF168514	BF168514 601775412
3	230.4	56.9	769	144	BF168856	BF168856 601775314
4	226.6	56.0	768	114	AM403591	AM403591 UI-HF-BKO
5	226.6	56.0	764	150	BF580556	BF580556 602097359
6	226	55.8	911	165	BE286958	BE286958 601092470
7	225.6	55.7	847	144	BF165486	BF165486 601777393
8	224.4	55.4	739	165	BE287568	BE287568 601097304
9	224.2	55.4	1093	171	BF974290	BF974290 602243946
10	224.2	55.4	1093	171	BF974290	BF974290 602243946
11	224	55.3	417	115	AM408371	AM408371 UI-HF-BKO
12	223	55.1	889	144	BF134160	BF134160 601778840
13	220.8	54.5	477	171	BF975791	BF975791 602246355
14	220.8	54.5	488	102	AI791363	AI791363 oh88a09.Y
15	220.8	54.5	494	172	BG060202	BG060202 nah49410.
16	220.8	54.5	698	150	BF584024	BF584024 602096264
17	220.8	54.5	849	150	BF582051	BF582051 602099230
18	220.8	54.5	1012	171	BF974633	BF974633 602243363







SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 911)  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Lohar Hemighausen Ph.D., Robin Humphreys  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM524 row: k column: 18  
High quality sequence stop: 688.  
Location/Qualifiers  
1. 911  
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/lab\_host="DH10B"  
/note="Organ: mammary; Vector: PCMV-SPORT6, Site:1; Salt;  
Site:2; NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Lohar Hemighausen/Robin Humphreys,  
NIH"

BASE COUNT 190 a 262 c 261 g 197 t 1 others  
ORIGIN

Query Match 55.8%; Score 226; DB 165; Length 911;  
Best Local Similarity 75.2%; Pred. No. 9.3e-58;  
Matches 310; Conservative 0; Mismatches 95; Indels 7; Gaps 2;

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DB 8 ATGGAGTGGAGCTGTATCATGCTCTCTCTGGCAGCACAGCTACAGGTGCCACTCCAG 67  
QY 61 gtccagctgtgtcagctgtgtggtcgtgaagagctgtgagctcagtgaaagtgtcc 120  
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DB 68 GTCCAACTGACAGCCTTG6G6CTGTGTGAAGCCTG6GCTTCACTAAAGCTGTCC 127  
QY 121 tgcacagcttcgcgctacacattcaactgattatgctacagtgatgtg-agaacagcttc 179  
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DB 128 TGCAGAGCTTCTGTGCTACACCTTACCAAGTTACGATGCACCTGGTGAACGACAGGCC 187  
QY 180 tgcacagggcctcgtgagtgtgattatlaatactactatgataataacaaactaca 239  
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DB 188 TGCAGAGGCTTGTGAGTGTGAAGATTGATCTAATAGTGTGCTACTAAGTACAA 247  
QY 240 ccggaatttcaaggaagcacaatgactgtgacaaagtgcagcagcagcactatat 299  
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DB 248 TGAAGAAATTCAAGAGCAAGGCCACACTGACTGTAGACAAACCTCCAGCAGCTACAT 307  
QY 300 ggaactagttcttctgtgagctgtgagatacggcgttattactgttcaagagcggtcgt 359  
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DB 308 GCAGCTCAGCAGCTGTGATGTGAGACTGTGCGGTCTATTACTGTCAAGAGGGGGGA 367  
QY 360 gta-----tatggaactactgtgggttcaaggtaacctgttcaacgcttcccta 405  
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DB 368 TTACGAGCGTATGAGCTACTGTGGGTCAAGGAACCTCAGTACGCTGTCCCTCA 419

RESULT 7\*

BF165486  
LOCUS BF165486 847 bp mRNA EST 30-OCT-2000  
DEFINITION 60177333F1 NCI\_CGAP\_Lu29 Mus musculus CDNA clone IMAGE:4019039 5',  
mRNA sequence.  
ACCESSION BF165486  
VERSION BF165486.1 GI:11045851  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 847)  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9270 row: i column: 24  
High quality sequence stop: 760.  
Location/Qualifiers  
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Stem cell origin."  
/lab\_host="DH10B"  
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Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

BASE COUNT 179 a 223 c 242 g 203 t  
ORIGIN

Query Match 55.7%; Score 225.6; DB 144; Length 847;  
Best Local Similarity 73.8%; Pred. No. 1.2e-57;  
Matches 301; Conservative 0; Mismatches 104; Indels 3; Gaps 1;

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DB 74 GTTGTGTTGAAGCGTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGCTC 133  
QY 121 tgcacagcttcgcgctacacattcaactgattatgctacagtgatgtg-agaacagcttc 180  
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QY 181 ggaacggcctcgtgagtgtgattatlaatactactatgataataacaaactacaac 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 194 GGACAGGGCTTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 253  
QY 241 cagaagtttaagggcacaagcacaatgactgtgacaaagtgcagcagcagcactatat 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 254 GAGAAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAACCTCCAGCAGCTACATG 313  
QY 301 ggaactagttcttctgtgagctgtgagatacggcgttattactgttcaagagcggtcgt 360  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 314 GAGCTCAGCAGCTGTGAGCTGTGAGCTGTGCGGTCTATTACTGTGCAAGGACTACAGT 373

QY 361 tata---tgaactactgggtcaaggtacacctgtcacgcgtccca 405  
DB 374 GTACACTGACTACTGGGGCCAAAGCAACACTATCACAGTCTCTCA 421

RESULT 8  
LOCUS BE287568 567 bp mRNA EST 26-OCT-2000  
DEFINITION 601097304F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:3495985 5',  
mRNA sequence.  
ACCESSION BE287568  
VERSION BE287568.1 GI:9166664  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 567)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHAM8547 row: h column: 02  
High quality sequence stop: 563.  
Location/Qualifiers  
1..567  
/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3495985"  
/clone\_lib="NCI\_CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;  
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Lothar Hennighausen/Robin Humphreys,  
NIH"

BASE COUNT 137 a 152 c 147 g 131 t  
ORIGIN

Query Match 55.4%; Score 224.4; DB 165; Length 567;  
Best Local Similarity 73.4%; Pred. No. 2.5e-57;  
Matches 304; Conservative 0; Mismatches 101; Indels 9; Gaps 1;

QY 1 atgggttggaactgtatcatctcttcttcgtgtaccacagctcagtgatcccg 60  
DB 17 ATGGATGAGCTCTATCATCTCTTCTTGATGCAACAGCTACAGGTCTCCACG 76  
QY 61 gtccagctgtgtcagctcgtgagctgagtgaaagccctggagctcagtgagtgctc 120  
DB 77 GTCCAACTGCACAGCCTTGCGGCTGAGCTGCTGAGGCTCGGAGTTTCATGAAGCTGCTC 136  
QY 121 tgcagaacttcggtctacacatctcgtatctgctatacagtggtgagacagctcct 180  
DB 137 TGCAGAGCTTCTGCTACTACCTCTTACACCGACTACTGGGTGAACCTGGTGAAGCAGAGGCT 196  
QY 181 ggaagggccctcagtgatgattgagttatataattactatgataataacaactaac 240  
DB 197 GGACAGGCTTGTGAGTGTGATGATTCATCTCCGATGAGTGAATTTAGTTAGTTAA 256  
QY 241 cagaagtttaagggcaagggccacaatgactctgagacaagtcgacagacagcctatag 300

DB 257 CAGAAGTTTAAGCAAGAGCCACATTTAGCTGTAGCAAAATCTCCAGCAGACCTATCATG 316  
QY 301 gaacttagtctcttgagatctgaagataagccgtttattactgtgcaagagcgctcg 360  
DB 317 CAACTCAGAGCCCGCAGCATCTGAGAGCTGCGGTCTATTACTGTGCAAGAGCGAGCGC 376  
QY 361 tatatggac-----tactgggtcaaggtacacctgtcacgcgtccca 405  
DB 377 TACGTAGACTGTTATTATTATTGGGCCAAGGAGACTCTGTCTCTCTGCA 430

RESULT 9  
LOCUS BE284158 739 bp mRNA EST 13-JUL-2000  
DEFINITION 601099428F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3491766 5',  
mRNA sequence.  
ACCESSION BE284158  
VERSION BE284158.1 GI:9160900  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 739)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE Unpublished (1999)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHAM8536 row: h column: 07  
High quality sequence stop: 535.  
Location/Qualifiers  
1..739  
/organism="Mus musculus"  
/strain="CZECH II (fetal)"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3491766"  
/clone\_lib="NCI\_CGAP\_Lu29"  
/tissue\_type="spontaneous tumor, metastatic to mammary.  
stem cell origin."  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site:1: SalI;  
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

BASE COUNT 184 a 210 c 184 g 161 t  
ORIGIN

Query Match 55.4%; Score 224.2; DB 165; Length 739;  
Best Local Similarity 73.5%; Pred. No. 3.1e-57;  
Matches 302; Conservative 0; Mismatches 103; Indels 6; Gaps 1;

QY 1 atgggttggaactgtatcatctcttcttcgtgtaccacagctcagtgatcccg 60  
DB 13 ATGGATGAGCTCTATCATCTCTTCTTGATGCAACAGCTACAGGTCTCCACG 72  
QY 61 gtccagctgtgtcagctcgtgagctgagtgaaagccctggagctcagtgagtgctc 120  
DB 73 GTCCAACTGCACAGCCTTGCGGCTGAGCTGCTGAGGCTCGGAGTTTCATGAAGATGCTC 132  
QY 121 tgcagaacttcggtctacacatctcgtatctgctatacagtggtgagacagctcct 180  
DB 133 TGCAGAGCTTCTGCTACTACCTCTTACACAGCTATGATTAAGCTGGGTGAAGCAGAAACT 192

0y	181	gagacgggcccctgagatggatcttgagctcttaattacttactatgataatacaaacacac	240
Db	193	AGACAGGGCCCTTGATGCGATTGGACAGATTATTTCTCGAGATGGTGTACACTTACTACANT	252
0y	241	cagaagcttaagaggcaagccacaatgactctgtagacaagtcgacgagacacagcctata	300
Db	253	GAAAGTTCAAGAGCAAGGCCACACTGACTGCAGACAATCCTCCAGCACACACTTACATG	312
0y	301	gaactagttctttagatctgagatcagatcgcgcgtttactatctgtgcaaga-----gcg	354
Db	313	CAGCTCACACAGCCTGACATCTGAGGACCTCGAGCTCTATTTCTGTGCAAGATGGGGGAG	372
0y	355	gcctgtatctatgactactgaggctcaagctaccctctgcaacgcttcctca	405
Db	373	CCCTGGAGACGTGGACTACTGGGGCCCAAGGCACACTATTCACAGTCTCCTCA	423
RESULT 10			
BF974290			
LOCUS	6022439461	NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4335131 5'	
DEFINITION	mRNA sequence.		
ACCESSION	BF974290		
VERSION	BF974290.1	GI:12341505	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 1093)		
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Tel: (301) 486-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNI) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNI at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> Plate: LHCMI205 row: 1 column: 12 High quality sequence stop: 759. Location/Qualifiers 1. 1093 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4335131" /clone_lib="NIH_MGC_48" /tissue_type="Primary B-cells from tonsils (cell line)" /lab_host="DH10B (phage-resistant)" /note="Organ: B-cells; Vector: pCM8; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."		
BASE COUNT			
ORIGIN	281 a	330 c	299 g 183 t
Query: Match 55.4%; Score 224.2; DB 171; Length 1093; Best Local Similarity 73.5%; Pred. No. 3.4e-57; Matches 302; Conservative 0; Mismatches 103; Indels 6; Gaps 1;			
0y	1	gtggatggaactgatacatctcttcttggttaccacacagagtgtgcattccacg	60

Db	41	ATGACGTGCACCTGGAGATATCTCGTCTTGTTGGTCAGAGACCTACAGGACACCCAGGCCAG	100
OY	61	gtccaagtgtgtgcâgtcctcgtgggtctgaagtgaaagccctggagctcaagtgaagtgctc	120
Db	101	GTCCAGCTGTGATCAGTCTGGGGCTGTGAGTGTGAAGAACCTGGGGCTCTAGTGAAGTCTCC	160
OY	121	tgcagaattctccggtctaacacttaacttgattatgctataagatgggtggaaagggctcc	180
Db	161	TCCAAGGTTTCCCGCTATACACCTCTACTCAATTAATTCATATGCACTGGGTGCAACAGGGCTCT	220
OY	181	ggacagggccctcgatgtgatgtgaattataatacttaactatgaataaacaattacaac	240
Db	221	GGAAAGAGGCTTGAATGATGGAGTGTGGAGGTTTATCTGTCAAGCTGGTGAACAGCTTACGCA	280
OY	241	cagaagattlaaggycaagggcacacaatgactctgtagacaagtcgacagcgacagcctatag	300
Db	281	CAGAGTTCACGGGAGAGTCAACCATGACCGAGGACACATCTACAGACGCGCTTACATG	340
OY	301	gaacttagtctcttgagatcttgagatctgagatacggcgctttatactactgtgcaa-----gagcg	354
Db	341	GAGCTGACACACCTGAGATCTGACGACACGGGCGCTGTATTACTGTGCACACTTACCATGAT	400
OY	355	gacctgtatatagactactatgggtgcaagatgataccctgttaaccgctctctca	405
Db	401	ATTAGGGCTCTGACTTACTTGAGGCGCAGGGAACCTGTGGACCGTCTCTCA	451

FEATURES	SOURCE	LOCATION/Qualifiers
LOCUS	AM408371	417 bp mRNA
DEFINITION	UT-HF-BK0-abk-c-03-0-UT.r1 NIH_MGC-36	Homo sapiens cDNA clone
ACCESSION	AM408371	IMAGE:3056620 5', mRNA sequence.
VERSION	AM408371.1	GI:5927428
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Enxarxola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	1 (bases 1 to 417)	
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999)	
CONTACT	Robert Strausberg, Ph.D.	
TEL	(301) 496-1550	
EMAIL	Robert.Strausberg@nih.gov	
Eco RI site shown at the beginning of the sequence.		
Tissue Procurement	Louis M. Staudt, M.D., Ph.D.	
CDNA Library Preparation	M.B. Soares Lab	
CNA Library Arrayed by	M.B. Soares Lab	
DNA Sequencing by	M.B. Soares Lab	
Clone distribution	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLML at:	
www-bio.lnlml.gov/bdrrp/image/image.html		
Seq primer	M13 Forward.	
1. 417		
/organism="Homo sapiens"		
/db_xref="taxon:9606"		
/clone="IMAGE:3056620"		
/clone_lib="NIH_MGC_36"		
/tissue_type="lymph"		
/cell_type="germlinal center B cells"		
/cell_line="MGC85"		
/lab_host="DH10B (LTI)"		
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI; constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."		
91 a	106 c	130 g
		90 t





Site-2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 102 a 127 c 150 g 98 t

Query Match 54.5%; Score 220.8; DB 171; Length 477;  
Best Local Similarity 76.7%; Pred. No. 2.9e-56;  
Matches 270; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

1 atgggttggaactgtatcatctctcttcgtttacacagctcagtgagctccag 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
27 atggactggacgtgagagcttcttcttgggtggcagcagctcagctccag 86  
61 gtccagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgagct 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
87 gtgcacctgtgtgagctgtgagctgtgagctgtgagctgtgagctgtgag 146  
121 tgcgaagcttcggtcagctacatcattcattatgctatcagtgagctgtc 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
147 tgcgaagcttctgagagcttgcagctcagctcagctcagctcagctcag 206  
181 ggcagagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgag 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
207 ggcagagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgag 266  
241 cagaagcttcaagggcagaagcagctgtgagctgtgagctgtgagctgtgag 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
267 cagaagcttcaagggcagaagcagctgtgagctgtgagctgtgagctgtgag 326  
301 gaactagcttcttggagctgtgagctgtgagctgtgagctgtgagctgtgag 352  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
327 gacctgagcagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgag 378

RESULT 14  
LOCUS A1791363 488 bp mRNA EST 13-DEC-1999  
DEFINITION oh6a09.y5 NCI-CGAP Kids Homo sapiens cDNA clone IMAGE:1472152.5,  
similar to gb:1M8512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);,  
mRNA sequence.  
A1791363  
ACCESSION A1791363.1 GI:5339079  
VERSION A1791363.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 488)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Other ESTs: oh6a09.x5  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
cDNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

\* This read is a RESEQUENCE of a previously sequenced human clone

Original clone citation: see original entry for original citation  
Information  
This 5' resequenced clone has no previous 5' data to verify this  
new read against  
Insert Length: 1021 Std Error: 0.00  
Seq primer: 40RP from Gibco  
High quality sequence stop: 438.  
Location/Qualifiers

FEATURES  
source

1.488

/organism="Homo sapiens"  
/dbxref="taxon:9606"  
/clone="IMAGE:1472152"  
/clone\_lib="NCI-CGAP\_Kids"  
/tissue\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with  
a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
ACTGCAAGATTTCCGGCCGCAATATTTTATTTTATTTTATTTTATTTTATTTT  
3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 130 a 121 c 142 g 94 t 1 others

Query Match 54.5%; Score 220.8; DB 102; Length 488;  
Best Local Similarity 76.7%; Pred. No. 2.9e-56;  
Matches 270; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

1 atgggttggaactgtatcatctctcttcgtttacacagctcagtgagctccag 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
28 atggactggacgtgagagcttcttcttgggtggcagcagctcagctccag 87  
61 gtccagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgag 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
88 gtgcacctgtgtgagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgag 147  
121 tgcgaagcttcggtcagctacatcattcattatgctatcagtgagctgtc 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
148 tgcgaagcttctgagagcttgcagctcagctcagctcagctcagctcagctcag 207  
181 ggcagagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgag 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
208 ggcagagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgag 267  
241 cagaagcttcaagggcagaagcagctgtgagctgtgagctgtgagctgtgagctgtgag 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
268 cagaagcttcaagggcagaagcagctgtgagctgtgagctgtgagctgtgagctgtgag 327  
301 gaactagcttcttggagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgag 352  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
328 gacctgagcagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgag 379

RESULT 15  
LOCUS BG060202 494 bp mRNA EST 25-JAN-2001  
DEFINITION nah4910.y1 NCI-CGAP\_HN19 Homo sapiens cDNA clone IMAGE:425907.5,  
similar to TR:Q9Y298 Q9Y298 IIG VH PROTEIN PRECURSOR ;, mRNA  
sequence.  
BG060202  
ACCESSION BG060202  
VERSION BG060202.1 GI:12528447  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 494)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov

unknown library type  
Seq primer: -40RP from Gldco  
High quality sequence stop: 425.

## FEATURES

## SOURCE

Location/Qualifiers  
1..494  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4254907"  
/clone\_lib="NCI CGAP\_HN19"  
/tissue\_type="normal epithelium"  
/lab\_host="DH10B"  
/note="Organ: nasopharynx; Vector: pAMP10; mRNA made from normal nasopharyngeal epithelium, cDNA made by oligo-dT priming. Non-directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 500 bp. Primary library. cDNA library preparation: David B. Krizman, Ph.D. REFERENCE: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 132 a 123 c 143 g 96 t  
ORIGIN

Query Match 54.5%; Score 220.8; DB 172; Length 494;  
Best Local Similarity 76.7%; Pred. No. 2.9e-56;

Matches 270; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

```

OY 1 atgggttggaactgtatcatctctctctctctgttaccacagctacaggtgtgactccag 60
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33 ATGACCTGCACCTGCAGATCTCTCTTCTTGGCGACAGCTACAGCCACCCGCCAG 92

OY 61 gtccagctgtgcaagctctgaggctgaagaagcctggagctcagtggaagtgctc 120
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 93 GTCCAGCTGTACAGCTGTGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGTCTCC 152

OY 121 tgcagaagctccgcgtacacattcaatgatactatacagtggtgtagacaggtcct 180
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 153 TGCAGGTTTCGGATACACCTCCTACATGATTCATGCACTGGGTGGACAGGCTCCT 212

OY 181 gacagagcctcagatgagattgaattatattactatgataataaactacaac 240
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 213 GGAAGAGGCTTGAATGGATGGAGGTTTGTATCTGAAGATGCTGAACAATCTTACGCA 272

OY 241 cagaagtttaagggcaagccacaatgactgtagacaagtcgacgagcagcctatag 300
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 273 CAGAAGTTCAGAGGCGAGGTACACATGACCGAGACACATCTACAGACACAGCCTACATG 332

OY 301 gaacttagtctcttgagatctgagatagcagcgcttattactctgcaagag 352
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 333 GAGCTGACAGCCTGAGATCTGAGACACAGCGCGCTGATTTACTGTGCAACAG 384

```

Search completed: April 29, 2001, 20:11:00  
Job time: 4367 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 19:41:33 ; Search time 151.39 Seconds  
(without alignments)  
1561.737 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405  
Sequence: 1 atgggttgacgtatcatc.....ccctgtcacccgtctctca 405

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

N.Geneseq\_0401:\*

- 1: /SIDS2/gcgdata/geneseq/geneseq/NA1980.DAT:\*
- 2: /SIDS2/gcgdata/geneseq/geneseq/NA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseq/NA1982.DAT:\*
- 4: /SIDS2/gcgdata/geneseq/geneseq/NA1983.DAT:\*
- 5: /SIDS2/gcgdata/geneseq/geneseq/NA1984.DAT:\*
- 6: /SIDS2/gcgdata/geneseq/geneseq/NA1985.DAT:\*
- 7: /SIDS2/gcgdata/geneseq/geneseq/NA1986.DAT:\*
- 8: /SIDS2/gcgdata/geneseq/geneseq/NA1987.DAT:\*
- 9: /SIDS2/gcgdata/geneseq/geneseq/NA1988.DAT:\*
- 10: /SIDS2/gcgdata/geneseq/geneseq/NA1989.DAT:\*
- 11: /SIDS2/gcgdata/geneseq/geneseq/NA1990.DAT:\*
- 12: /SIDS2/gcgdata/geneseq/geneseq/NA1991.DAT:\*
- 13: /SIDS2/gcgdata/geneseq/geneseq/NA1992.DAT:\*
- 14: /SIDS2/gcgdata/geneseq/geneseq/NA1993.DAT:\*
- 15: /SIDS2/gcgdata/geneseq/geneseq/NA1994.DAT:\*
- 16: /SIDS2/gcgdata/geneseq/geneseq/NA1995.DAT:\*
- 17: /SIDS2/gcgdata/geneseq/geneseq/NA1996.DAT:\*
- 18: /SIDS2/gcgdata/geneseq/geneseq/NA1997.DAT:\*
- 19: /SIDS2/gcgdata/geneseq/geneseq/NA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	405	100.0	405	21	A59694	DNA encoding heavy
2	334.6	82.6	405	21	A59692	Nucleotide sequence
3	277.2	68.4	524	12	Q14802	Encodes murine anti
4	277.2	68.4	524	12	Q14652	R6-5-D6 anti-ICAM-
5	272.2	67.2	446	11	Q05554	Sequence encoding
6	265.8	65.6	1767	19	V61363	Anti-human Fas hum
7	265.8	65.6	1767	21	A78271	Anti-human Fas hum
8	265.8	65.6	1768	19	V61364	Anti-human Fas hum
9	265.8	65.6	1768	21	A78272	Anti-human Fas hum
10	254.4	62.8	424	17	T42717	HumC3 VH coding se
11	253.6	62.6	451	15	O66702	DRG-200 Humanized

12	253.6	62.6	2071	19	V70080	Anti-Fas humanised
13	253.6	62.6	2071	21	A72184	DNA encoding human
14	253.6	62.6	2071	21	A11622	Humanised HE7A de
15	252	62.2	2073	21	A11644	Humanised anti-Fas
16	252	62.2	2073	21	A11645	Humanised anti-Fas
17	251.6	62.1	423	21	D00905	Humanised antibody
18	250.4	61.8	2073	21	A11646	Humanised anti-Fas
19	248.8	61.4	457	19	V70104	Humanised anti-Fas
20	248.8	61.4	457	21	A72146	Humanised anti-Fas
21	248.8	61.4	457	21	A11584	Humanised anti-Fas
22	248.8	61.4	2077	19	V70079	Humanised anti-Fas
23	248.8	61.4	2077	21	A72159	DNA encoding human
24	248.8	61.4	2077	21	A11597	Humanised HE7A de
25	248.2	61.3	405	21	A59698	DNA encoding heavy
26	245.6	60.6	2077	21	A11655	Humanised anti-Fas
27	245.2	60.5	423	21	D00907	Humanised antibody
28	245	60.5	405	20	V33947	Anti-CD33 antibody
29	245	60.5	411	21	A48845	CDNA encoding huma
30	244.8	60.4	409	21	287738	Anti-human VEGF re
31	243.4	60.1	405	19	V37264	CDNA encoding a va
32	243.4	60.1	405	21	295282	IgM chimeric antib
33	243.4	60.1	1773	18	T88869	H chain subunit of
34	243.4	60.1	1773	19	V66735	Anti-human Fas mon
35	243.4	60.1	1773	21	A78202	Anti-human Fas ant
36	242.2	59.8	478	20	V88433	EST clone GP196.
37	241.8	59.7	433	13	Q24790	Anti-Fas antibody
38	240.8	59.5	421	18	T73624	CDNA for humanised
39	240.2	59.3	443	10	N91820	DNA sequence of th
40	240	59.0	409	21	287778	Anti-human VEGF re
41	239	59.0	418	19	V59116	HML-24 antibody he
42	239	59.0	418	19	V07581	Anti-human HML-24
43	239	59.0	418	19	V39405	Humanised anti-HM1
44	239	59.0	418	19	V39350	Humanised anti-HM1
45	239	59.0	418	19	V39357	Humanised anti-HM1

#### ALIGNMENTS

RESULT	1
ID	A59694 standard; DNA: 405 BP.
XX	
AC	A59694;
XX	
DT	14-NOV-2000 (first entry)
XX	
DE	DNA encoding heavy chain variable region of humanised 3s1 antibody.
XX	
KW	Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW	autoimmune disease; infectious disease; inflammatory disorder;
KW	systemic lupus erythematosus; diabetes mellitus; asthma;
KW	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW	multiple sclerosis; transplant rejection; proliferative disease;
KW	leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW	aplastic anaemia; myeloid dysplasia syndrome; ss.
XX	
OS	Synthetic.
OS	Mus sp.
OS	Homo sapiens.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..405
FT	/tag= a
FT	/product= "heavy chain variable region of 3D1 antibody"
FT	/note= "no termination codon given"
FT	1..57
FT	sig_peptide
FT	/tag= b
FT	mat_peptide
FT	58..405
FT	/tag= c
XX	
PN	WO200047625-A2.
XX	

PD 17-AUG-2000.  
 XX 09-FEB-2000; 2000WO-US03303.  
 XX 12-FEB-1999; 99US-0249011.  
 PR 24-JUN-1999; 99US-0339596.  
 XX (GEMV ) GENETICS INST INC.  
 PA  
 XX Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX WPI: 2000-524532/47.  
 DR P-PSDB; B07965.  
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-1524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 XX  
 PS Example 3; Fig 2A; 162pp; English.  
 XX  
 CC The present sequence encodes the heavy chain variable region of the  
 CC humanised murine antibody 3D1. The antibody has a binding specificity to  
 CC B7 molecules. The antibody is used to construct humanized  
 CC immunoglobulins, which comprise an antigen binding region of non-human  
 CC origin and a portion of a human immunoglobulin. The humanized  
 CC immunoglobulins are useful for treating autoimmune diseases, infectious  
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 CC  
 XX Sequence 405 BP; 102 A; 88 C; 110 G; 105 T; 0 other;  
 SO

Query Match 100.0%; Score 405; DB 21; Length 405;  
 Best Local Similarity 100.0%; Pred. NO. 3.9e-102;  
 Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgggttggaactgatatctctctctctggtaccacagctcaggtgacactccag 60  
 DB 1 atgggttggaactgatatctctctctctggtaccacagctcaggtgacactccag 60  
 QY 61 gtccagctggtgcagctctggtggtcgaaggcctggagctcagtggaagtgctc 120  
 DB 61 gtccagctggtgcagctctggtggtcgaaggcctggagctcagtggaagtgctc 120  
 QY 121 tgcagaagcttcgcgtacacattcattatgatactgatacagtggtgagaagctcct 180  
 DB 121 tgcagaagcttcgcgtacacattcattatgatactgatacagtggtgagaagctcct 180  
 QY 181 ggaacggcctcgaagtggaattggaatttaataattactgatacaatacaaacacac 240  
 DB 181 ggaacggcctcgaagtggaattggaatttaataattactgatacaatacaaacacac 240  
 QY 241 cagaagtttaaggcgaagccacaatgactgtagacaagtcgacgacagccatata 300  
 DB 241 cagaagtttaaggcgaagccacaatgactgtagacaagtcgacgacagccatata 300  
 QY 301 gaactacttcttgagttctgagatagatagcgcttacttctgcaagagcggtcgg 360  
 DB 301 gaactacttcttgagttctgagatagatagcgcttacttctgcaagagcggtcgg 360  
 QY 361 tatatgactactggtgcaagtgacacctgtcacgctcctca 405  
 DB 361 tatatgactactggtgcaagtgacacctgtcacgctcctca 405

RESULT 2  
 ID A59692 standard; DNA: 405 BP.  
 AC A59692;  
 XX 14-NOV-2000 (first entry)  
 DE Nucleotide sequence of heavy chain variable region of 351 antibody.  
 XX  
 KW Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;  
 KW autoimmune disease; infectious disease; inflammatory disorder;  
 KW systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;  
 KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;  
 KW multiple sclerosis; transplant rejection; proliferative disease;  
 KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;  
 KW aplastic anaemia; myeloid dysplasia syndrome; ss.  
 KW  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..405  
 FT /\*tag- a  
 FT /product= "heavy chain variable region of 3D1 antibody"  
 FT /note= "no termination codon given"  
 FT sig\_peptide 1..157  
 FT /\*tag- b  
 FT mat\_peptide 58..405  
 FT /\*tag- c  
 XX  
 PN WO200047625-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PR 09-FEB-2000; 2000WO-US03303.  
 PR 12-FEB-1999; 99US-0249011.  
 PR 24-JUN-1999; 99US-0339596.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 XX Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX WPI: 2000-524532/47.  
 DR P-PSDB; B07963.  
 XX  
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-1524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 XX  
 PS Example 1; Fig 1A; 162pp; English.  
 XX  
 CC The present sequence encodes the heavy chain variable region of the  
 CC murine antibody 3D1. The antibody has a binding specificity to B7  
 CC molecules. The antibody is used to construct humanized immunoglobulins,  
 CC which comprise an antigen binding region of non-human origin and a  
 CC portion of a human immunoglobulin. The humanized immunoglobulins are  
 CC useful for treating autoimmune diseases, infectious diseases,  
 CC inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 CC  
 XX Sequence 405 BP; 110 A; 89 C; 102 G; 104 T; 0 other;  
 SO

Query Match

82.6%; Score 334.6; DB 21; Length 405;

```

Post,Local Similarity 89.18; Pred.No. 8.2e-83;
Matches 361; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

```

OY	1	atgggttcggaactatcacatctcttccttggtacccaacatacaagctgagcactccag	60
Db	1	atgggttcggaactatcacatctcttccttggtacccaacatacaagctgagcactccag	60
OY	61	gtccagactcgtgtgcagctctgggctggaagtcgaagagcctcgtggagctcagtgtgaagtgtccc	120
Db	61	gtccagactcgtgcagctctgggctggaagtcgaagagcctcgtggagctcagtgtgaagtgtccc	120
OY	121	tgcgaagcttcctcggtctacacattcacatgatactatgaatgtggtgtgagacagctcct	180
Db	121	tgcgaagaggtcttcgggtctacacattcacatgatactatgaatgtggtgtgagacagagttcat	180
OY	181	ggaacaggccctccagcttgatctgagatctatataatttaccatctatataataacactcaaac	240
Db	181	gcaaaagagctctagagctggtatctggatctatcaatttaccatctatataataataacactcaaac	240
OY	241	cagaagatttaagaggcacaagggccacaatgactgttagacaagctgcagcgacagcctatag	300
Db	241	cagaagatttaagaggcacaagggccacaatgactgttagacaatctctccagcagcctatag	300
OY	301	gaacttcgtctcttggagaatctgaaagatacagcgcttattatctcgtctgcagaagcgcgcttg	360
Db	301	gaacttcgcagatgtacaatctgaaagatacttcgtccatctattactggtgcagaagcgcgcttg	360
OY	361	tatatgactactcgtgggttcgaagtaagtaacctgttcaacgcttcctcca	405
Db	361	tatatgactactcgtgggttcgaagtaagtaacctcagcttcgcttcctcca	405

### RESULT 3

ID Q14802 standard; DNA; 524 BP.

AC Q14802;

DT 13-FEB-1992 (first entry)

DE Encodes murine anti-ICAM monoclonal antibody heavy chain

KM intercellular adhesion molecule; V(H); mouse;  
KW R6-5-D6 murine MAb; complementarity determining region; CDR; ds

05 Mus musculus.

FH	Key	Location/Qualifiers
FM	stc non+idc	34 80

```

/*tag= a
/standard name= leader

```

PN W09116927-A.

PD 14-NOV-1991.

PF 29-APR-1991; 91WO-US02942.

PR 27-APR-1990; 90GB-0009549.

PA (CELL-) CELLTECH LTD.  
PA (BOEH) BOEHRINGER INGELHEIM PHA

PI Adalr JR, Athwal DS, Rothlein RA;

DR WPI; 1991-353533/48.  
DR P-PSDB; R15060.

PT New humanised CDR-grafted anti-ICAM antibodies - used to treat PT and prevent inflammation (e.g. psoriasis) tumours, viral PT infections and asthma and in diagnosis

XX .  
PS Disclosure; Fig 2; 83pp; English.

CC The heavy chain sequence was isolated from a cDNA library prep. from  
CC hybridoma cell line R6-5-D6 which secretes murine IgG2a/kappa  
CC antibody. The library was screened using a 980bp BamHI-EcoRI  
CC fragment of a previously isolated mouse IgG2a constant region  
CC clone. The murine framework-encoding sequences (i.e. not encoding  
CC CDRs) will be replaced by human framework sequences to produce  
CC recombinant (CDR-grafted humanised) antibody molecules having  
CC specificity for ICAM-1.

50 Sequence 524 BP; 128 A; 130 C; 135 G; 131 T; 0 other;

Query Match	68.4%;	Score 277.2;	DB 12;	Length 524;
Best Local Similarity	81.4%;	Pred. No. 5e-67;		
Matches 337;	Conservative 0;	Mismatches 68;	Indels 9;	Gaps 1.

QY 1 atgggtctggaactgacatcatctctctctgtgttccacacagctaaaggtgagactccag 60  
 Db 34 atgggtctggaactgacatcatctctctctgtgttccacacagctaaaggtgagactccag 93  
 QY 61 gtccacgcctgctgacagctctcgtgggtctgaggttgagaagacgcctggaagctaaagtgtcc 120  
 Db 94 gtccacgcctgacagcaagctctcgtgggtctgaggttgagaagacgcctggaagctaaagtgtcc 153  
 QY 121 tgcgaagcttcgcgcgtacacattcaactgatatgtctatacaagctgtggtgtgagaacagctcct 180  
 Db 154 tgcgaaggtctccgcgtacacattcaattgatatgtctatacaactgtggtgagaagagagttcat 213  
 QY 181 ggaacgggcgcctcgaattgattggaggttaattatattactatgttgaaatacaaaactaaac 240  
 Db 214 gcaaaagagctcagaagatgagatttggagttatagatgtcttaactctggtgacacaaactaaac 273  
 QY 241 cagaaggtttaaagggtgaagagccacacatgactgtagaacaagctgcgaagagcacagcctatag 300  
 Db 274 cagaaggtttaaagggtgaagagccacacatgactgtagaacaatctcccaacacagcctattg 333  
 QY 301 gaacttagtctcttgagagctcgtagagatacgggcgtttaattactgtgtcgaagagcggcctgg 360  
 Db 334 gaacttgcagaattgactcctgtagagatattctgcatactattactgtgcnaagaggggagatgg 393  
 QY 361 -----tataagactatgggtgaagaagaatgacaccttgcagacgctcctca 405  
 Db 394 ttactactctccttggactacttgggtggaaggaacaccttccaaagtctcctca 447

RESULT	4
Q14652	

AC Q14652;

DT 14-FEB-1992 (first entry)

DE R6-5-5-D6 anti-ICAM-1 heavy chain.

KW Intercellular adhesion molecule-1; antibody; chimaeric; ds.

OS Mus musculus.

	key	Location/Qualifiers
FH	sig_peptide	34..90
FT		

PN W09116928-A

PD 14-NOV-1991

PF 29-APR-1991; 91WO-US02946.

[illegible][illegible]



QY 301 gaactagctcttgaagatcgaagatacagcggttattactgtgcgaagcgcctcg 360  
||||| ||| ||||| ||| ||| ||||| ||||| |||  
Db 345 gaactgcagactgtacatcgaagatctcgcacatctactgtgcgaaga---ggaagc 401  
QY 361 tatatgactactggggtcgaaggtacccctgtcacccgtctcctca 405  
- ||||| ||||| ||| ||| ||||| |||||  
Db 402 aacctgactactcgtggcgaagcaccacatctcacagctctcctca 446

## RESULT 6

V61363  
ID V61363 standard; cDNA to mRNA; 1767 BP.

AC V61363;

DT 18-JAN-1999 (first entry)

XX Anti-human Fas humanised antibody CH11 heavy chain HmuH cDNA.

XX Humanised antibody: Fas; CH11: monoclonal antibody: MAb: apoptosis;

KW autoimmune disease; rheumatoid arthritis; therapy: human;

KX antibody engineering; ds.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT sig\_peptide 1..57

FT mat\_peptide 58..1764

FT /\*tag= a

FT /\*tag= b

PN EP866131-A2.

PD 23-SEP-1998.

PF 20-MAR-1998; 98EP-0302113.

PR 21-MAR-1997; 97JP-0067938.

XX (SANY ) SANKYO CO LTD.

XX Hatuyama H, Nakahara K, Serizawa N, Takahashi T;

PI Yonehara S;

XX WPI: 1998-482965/42.

DR P-PSDB: W71880.

XX Production of anti-Fas protein humanised antibodies - for use in

PT inducing apoptosis on Fas expressing cells in the treatment of

PT autoimmune diseases, especially rheumatoid arthritis

XX Example 3; Page 103-105; 187pp; English.

XX This cDNA sequence codes for a humanised anti-Fas antibody CH11

CC heavy chain (see W71880), designated HmuH. HmuH is based on the

CC light chain (see W71888) of murine anti-human Fas monoclonal

CC antibody CH11. The humanised sequence was designed following

CC selection of donor residues from CH11 to be grafted onto acceptor

CC molecule 21.28'CL. 2 light chain sequences (see W71880-81) have

CC been designed, and each can be used in combination with any of 4

CC light chain sequences (see W71876-79) to provide novel, claimed

CC humanised CH11 IGM antibodies that lack a J chain. These humanised

CC anti-human Fas antibodies are capable of inducing apoptosis in cells

CC expressing Fas (e.g. synovialocytes) and are useful in the treatment

CC of autoimmune disease and chronic rheumatoid arthritis. DNA

CC sequences encoding the humanised antibodies are claimed, as are

CC vectors such as pMmuH5-1 including the HmuH nucleotide sequence,

CC and host cells such as Escherichia coli pMmuH5-1 (FERM BF-5863).

CC Sequence 1767 BP: 384 A; 568 C; 485 G; 330 T; 0 other;

Query Match 65.6%; Score 265.8; DB 19; Length 1767;  
Best Local Similarity 78.5%; Pred. NO. 9,3e-64;  
Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1 atgggttgaaactgtatcatctctctctgtttacacagctacagtggtgactccag 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1 atgggttgaaactgtatcatctctctctctgtttacacagctacagtggtgactccag 60  
1 atgggttgaaactgtatcatctctctctctgtttacacagctacagtggtgactccag 60  
QY 61 gtccagctgtgacgtctggtggtgagtgaaagacccgtggagctcagtgaaagtgtcc 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 61 gtccagctgtgacgtctggtggtgagtgaaagacccgtggagctcagtgaaagtgtcc 120  
121 tgcagaagcttcggctacacattcactgtattatgctatagctggtgagacagctcct 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 121 tgcagaagcttcggctacacattcactgtattatgctatagctggtgagacagctcct 180  
181 ggcagaggtcctcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 181 ggcagaggtcctcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240  
181 ggcagaggtcctcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240  
QY 241 cagaagtttaagggcagaagcacaatgactgtagacaagtcgacgacacataatg 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 241 cagaagtttaagggcagaagcacaatgactgtagacaagtcgacgacacataatg 300  
301 gaactagctcttgaagatcgaagatacagcggttattactgtgcgaagcgcctcg 360  
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 301 gaactagctcttgaagatcgaagatacagcggttattactgtgcgaagcgcctcg 360  
361 tatatgactactggggtcgaaggtacccctgtcacccgtctcctca 405  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 361 tatatgactactggggtcgaaggtacccctgtcacccgtctcctca 405

## RESULT 7

A78271  
ID A78271 standard; DNA; 1767 BP.

AC A78271;

DT 16-NOV-2000 (first entry)

XX Anti-human Fas immunoglobulin M heavy chain DNA sequence SEQ ID #85.

XX Antirheumatic agent; immunoglobulin M; IGM: apoptosis inducer;

KW immunosuppression; autoimmune disease; treatment: Rheumatism;

KX anti-Fas antibody; ss.

OS Synthetic.

PN JP2000154149-A.

PD 06-JUN-2000.

PF 17-SEP-1999; 99JP-0263984.

PR 18-SEP-1998; 98JP-0264598.

XX (SANY ) SANKYO CO LTD.

XX WPI: 2000-454476/40.

DR P-PSDB: B12917.

XX Anti-human Fas humanizing antibody-containing antirheumatic agents -

XX Example 2; Page 73-75; 109pp; Japanese.

XX The present invention relates to antirheumatic agents which comprise as

CC active ingredients an immunoglobulin M (IGM) protein. The IGM protein

CC does not include a J segment, has apoptosis inducing activity, and

CC consists of a light and heavy chain polypeptide produced synthetically.

CC The agents of the invention exhibit antirheumatic and immunosuppressive

CC activity and can be used to treat autoimmune diseases, especially

CC rheumatism. The IGM molecule used in the invention has human Fas-antigen



Db .361 gctatgactactgaggccagggaacctgctacacctctccta 405

RESULT 9

A78272 standard; DNA: 1768 BP.

AC A78272:

DI 16-NOV-2000 (first entry)

DE Anti-human Fas immunoglobulin M heavy chain DNA sequence SEQ ID #87.

KW Antirheumatic agent; immunoglobulin M; Igm: apoptosis inducer;

KW immunosuppression; autoimmune disease; treatment; rheumatism;

KM anti-Fas antibody; ss.

OS Synthetic.

PN JP2000154149-A.

PD 06-JUN-2000.

PF 17-SEP-1999; 99JP-0263984.

PR 18-SEP-1998; 98JP-0264598.

PA (SANY ) SANKYO CO LTD.

DR WPI: 2000-454476/40.

DR P-PSDB; B12918.

PT Anti-human Fas humanizing antibody-containing antirheumatic agents

PS Example 2; Page 77-79; 109pp; Japanese.

CC The present invention relates to antirheumatic agents which comprise as  
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
CC does not include a J segment, has apoptosis inducing activity, and  
CC consists of a light and heavy chain polypeptide produced synthetically.  
CC The agents of the invention exhibit antirheumatic and immunosuppressive  
CC activity and can be used to treat autoimmune diseases, especially  
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
CC binding properties. Included in the invention are nucleotide sequences of  
CC the IgM light and heavy chains (see A78267-A78272) and the corresponding  
CC protein sequences (see B12913-B12918 and B12919), and nucleotide  
CC sequences of the humanised anti-human Fas Ig CH11 (see A78202-A78206) and  
CC antibody CDR peptides (B12902-B12907). Also included are anti-human Fas  
CC anti-human Fas antibody, light, heavy and kappa chains used in the  
CC invention are represented by sequences A78213-A78266. Primers used for  
CC sequencing the human Ig DNA used in the invention are represented by  
CC sequences A78277-A78318 and A78335-A78337, while humanised anti-Fas Ig  
CC DNA sequencing primers are represented by sequences A78321-A78334 and  
CC A78338-A78367. Primer sequences A78207-A78212 are specific for murine Ig  
CC DNA, and are used in the production of the agent of the invention.

CC Sequence 1768 BP: 387 A; 564 C; 485 G; 332 T; 0 other;

Query Match 65.6%; Score 265.8; DB 21; Length 1768;

Best Local Similarity 78.5%; Pred. No. 9.3e-64;

Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

OY 1 atgggttggaactatcatctctctctgttacacagctacaggtgtgactccag 60

DB 1 atggatgagagctgactctctctctctcctgcagacagcagcgctccactctg 60

OY 61 gtcacgctggtgacgtctgggctgagtggaagagccctggagctcagtagagttcc 120

DB 61 gtcacgctggtgacgtctgggctgagtggaagagccctggagctcagtagagttcc 120

OY 121 tgcagaagcttcgagctacacatcagtattatgtatatacagtggtgagacagctcct 180

DB 121 tgcagaagcttcgagctacacatcagtattatgtatatacagtggtgagacagctcct 180

OY 181 ggcacagggcctcgcagtgagtgagtgatttaattactatgataatacaactacaac 240

DB 181 ggcacagggcctcgcagtgagtgagtgatttaattactatgataatacaactacaac 240

OY 241 cagaagtttaagggcagaagcccaatgactgtagacaagtgacagacagcactatag 300

DB 241 cagaagtttaagggcagaagcccaatgactgtagacaagtgacagacagcactatag 300

OY 301 gaactagttcttgcagctcagatagatacagcgcttattactgtcgaagcggcctg 360

DB 301 gacgtgagagcagctgagatctgaagaacagcgctgtgattactgtgcgagaagttactat 360

OY 361 tatatgactactgggtggtcaagtaacctgtcacgcgtctccta 405

DB 361 gctatgactactgaggccagggaacctgctacacctctccta 405

RESULT 10

T42717

ID T42717 standard; DNA: 424 BP.

AC T42717:

XX 04-FEB-1997 (first entry)

DE HumC3 VH coding sequence.

XX Humanised antibody; variable heavy region; buried residue modification;

KW VH; HumC3 VH; BA46 antigen; human; milk fat globule; HMFG; lactation;

KW fat globule membrane; murine; mammary; epithelial cell; breast cancer;

KW breast membrane glycoprotein; therapy; immunotherapy; ss.

OS Synthetic.

XX Key Location/Qualifiers

FT CDS 11..418

FT /tag= a

FT /product= HumC3 VH (BR-M version)

PD W09608565-A2.

XX 21-MAR-1996.

PF 14-SEP-1995; 95WO-US11683.

PR 07-JUN-1995; 95US-0487598.

PR 16-SEP-1994; 94US-0307868.

PA (CANC-) CANCER RES FUND CONTRA COSTA.

PI Certianl RI, Do Couto FJR, Peterson JA;

DR WPI: 1996-179941/18.

XX P-PSDB; W06442.

PT Recombinant MC3 antibody which binds BA46 antigen of HMFG -

PT comprises a modified heavy or light chain variable region, useful in

PT the diagnosis and therapy of breast cancer

PS Claim 13; Fig 18; 91pp; English.

XX This sequence represents the coding sequence for the variable heavy (VH)

XX chain of the humanised murine antibody HumC3 VH. The MC3 VH sequence was

XX humanised using the buried residue modification technique, where

XX important non-human framework residues are unaffected. The MC3 antibody

XX binds to the BA46 antigen of the human milk fat globule (HMFG). The milk

XX fat globule membrane is derived from the apical surface of the mammalian

XX epithelial cell during lactation, and therefore is a source for breast

XX membrane glycoproteins. The antibody can be used in an in vitro method

XX to detect a HMFG antigen (or antigen fragment), and to diagnose the



CC	PCR amplification (see V70115-17), and includes humanising R44G
CC	and A/T67 amino acid substitutions. Host cell Escherichia coli
CC	pGHADH9V SANK 7029d harbors plasmid pGHADH9V carrying a fusion
CC	fragment of the humanised HV type HFE7A heavy chain and DNA
CC	encoding human IgM constant region, and is deposited as
CC	FERM BF-6273 (claimed). The invention provides methods for
CC	producing humanised antibodies by culturing host cells. Humanised
CC	versions of HFE7A (see W83031-37), like native HFE7A, are capable
CC	of inducing apoptosis in abnormal cells expressing Fas, and of
CC	inhibiting Fas-induced apoptosis in normal cells. The humanised
CC	antibodies are used to evaluate, in animal models, treatments of
CC	diseases that involve Fas/Fas ligand interactions, and also to
CC	treat such diseases, including autoimmune disease (e.g., systemic
CC	lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC	Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC	Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
CC	autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC	multiple sclerossis, Basedow's disease, thrombopenia purpura and
CC	insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC	myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC	anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX	
XX	
Seq	Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;
Query Match	62.6%; Score 253.6; DB 19; Length 2071;
Best Local Similarity	77.6%; Pred. No. 2..2e-60;
Matches 326; Conservative	0; Mismatches 79; Indels 15; Gaps
OY	1 atgggttggaactgctatcatccttcttcggttaccaagctacagtgtgcctccag 60
Db	21 atgggatggagctgtatactcctctcttctggttagacaacctaaagglytcccactcag 80
OY	61 gtccagctgtgcagctcgtagggctggaagcaagccggggagctccagtgaaagtgtcc 120
Db	81 gtccaactggtgctcagctctgggctgagttccaagaagcctggggcttcagtgaaagtgtcc 140
OY	121 tgcgaagcttcggctaccacattcgtattatgctacatacagtggltgagacaggtctcc 180
Db	141 tgcgaagcttcgctcacaccttcacacagctactgtagtcagtggtgtaaacaagccccct 200
OY	181 ggacagagcgctcctgagtgtgattatctaattactatgatatatacaaacataac 240
Db	201 ggcacgggctcttgagtgtgattgtgagagctgtacctctgtatgactactaactaat 260
OY	241 cgaagattaaaggcgaagccacaatgactgtgaaaagtgcagcgagcagactatg 300
Db	261 caaaagttcaaaggcaaggccacatgactgtgagaacatccactgcaagctacatg 320
OY	301 gaactagctctcttgagatctgagatcacggccgttatattactgtgtaaaaa----- 351
Db	321 gggctcagagcgtcgtgacatctgagacaagcgcgctctattactacgtgcaagaataaggac 380
OY	352 -----ggcgctggtatatagtaactcgtgggtcaagtaacctgtcacctgtcctoc 405
Db	381 tatagtaaacactgtaactcgtatgctcgtggggaaggaagcctgtgcacgcgtctoc 440
RESULT 13	
A72184	A72184 standard; DNA; 2071 BP.
AC	A72184:
XX	24-NOV-2000 (first entry)
DE	DNA encoding humanised anti-Fas antibody heavy chain, SEQ ID NO:116.
XX	
KW	Anti-Fas antibody: monoclonal antibody HFE7A; FERM-BP-5828;
KW	murine; humanised antibody; complementarity determining region; CDR;
KW	human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW	autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW	cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenias;





Db 383 tatagtaacaactggtactctgatatgtctggggccaaggtacaacttggtaaccgtctctctca 442

Search completed: April 29, 2001, 20:39:39  
Job time: 3486 sec

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cell 24, 625-637, 1981  
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: some  
A:Reference number: A90809; MUID:81234548  
A:Accession: A02038  
A:Molecule type: mRNA  
A:Residues: 1-137 <BOT>  
A:Cross-references: GB:000539; NID:g195118; PID:AAA8172.1; PID:g195119  
A:Note: the gamma-2a chain mRNA was cloned from a hybridoma making antibodies to the hAp  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-137/Product: Ig heavy chain V region (543) #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>  
F:118-122/Region: D segment  
F:123-137/Region: J segment (JH2)

[illegible]

RESULT 14  
F29380  
Ig heavy chain precursor V region (A003 40/567) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 23-Jul-1999  
C:Accession: F29380  
C:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.  
J. Biol. Chem. 262, 13579-13583, 1987  
A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable  
A:Reference number: A92612; MUID:86007582  
A:Accession: F29380  
A:Molecule type: mRNA  
A:Residues: 1-137 <CHE>  
A:Cross-references: GB:M7165; GB:J02815; NID:g195409; PID:AAA38294.1; PID:g195410  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin  
C:34-117/Domain: Immunoglobulin homology <IM>

Query Match	67.8%	Score 488	DB 2	Length 137
Best Local Similarity	69.6%	Pred. No. 8	1e-35	
Matches	96	Conservative	14	Mismatches 24; Indels 4; Gaps 2
OY	1	MGWNCILFEFLTATGATGVSQVOLVQSGAEVKKPGSSVKVSKASGCTFTFDYAIQWRQAP	60	
Db	1	MGWNTILFLVATGATGVSQVQVQPGALVLRPGISVLTSCASGCTNFTTYINNVKLRP	60	
OY	61	GQGLEWICIVNIYYDNTNYNQKFKGATGYVDKSTSTAYMELSSRSEDYAVYYCAR---	117	
Db	61	GQGLEWIEDIYPGSGSTNYNNEKFKATLVTDSSTAYMQLSSLSAEDSALYYCARQVG	120	
OY	118	AAAYMDYMGQGTLLTVSS	135	
Db	121	ETWFA-YWGQGTLLTVSA	137	

RESULT 15  
HVMST7  
Ig heavy chain precursor V region (TEPC 1017) - mouse

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C:Species: Mus musculus (house mouse)
C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 30-May-1997
C:Accession: A02033
R:Gilliam, A.C., Shen, A., Richards, J.E., Blattner, F.R.; Mushinski, J.F.; Tucker, F.
Proc. Natl. Acad. Sci. U.S.A. 81, 4164-4168, 1984
A:Title: Illegitimate recombination generates a class switch from C-mu to C-delta in
A:Reference number: A02033; MUID:84248078
A:Accession: A02033
A:Molecule type: mRNA
A:Residues: 1-138 <GIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig heavy chain V region (rePC 1017) #status predicted <MAT>
F:21-117/Region: V segment
F:34-117/Domain: immunoglobulin homology <IMM>
F:118-123/Region: D segment
F:124-138/Region: J segment

```

	Query Match	Best Local Similarity	67.7% Conservative	Score 487.5	DB 1	Length 138
	Matches 95		16	Mismatches 24	Indels 3	Gaps
Qy	1	MGWNCIIFFELVTTATGVHSQVQLVOSGAENVKPPSSVYKSCASGAYTFPTAYIDWVQAP				
Db	1	MGWSTIIIFLVAATPDVHSSQVQLPGAEIVKPPGASVQLSCASGCHFTYWIHWVQRP				
Qy	61	GQGELGICVNIYYDNTNNYNOKFFKGKATMYDKSTSIAYLSSLRSEDTIAYVYCARAAW				
Db	61	GQGLEWIEIENPDGRSNRYNEKFKNKATLVLDKSSSTAYMOLSSLTPEEFEEVAYVYCARSDG				
Qy	121	YMD---YWGQGLTVTVSS				
Db	121	YDMEFYVWGQGLTVTVFSA				

Search completed: April 25, 2001, 09:39:40  
Job time: 178 sec





```

RESULT 2
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BI-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL: J00529; AAA8170.1; -.
DR PIR; A02034; MKMS18.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 54 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC9F465 CRC64;

Query Match 69.68; Score 501; DB 1; Length 139;
Best Local Similarity 68.3%; Pred. No. 3.1e-43;
Matches 95; Conservative 16; Mismatches 24; Indels 4; Gaps 1;

QY 1 MGNACITFLVTTATGVSQVQVQSGAEVKKPGSSSVKYSCKASGYFTDTAIQWVQAP 60
DB 1 MGNWCMFLFAATATGVSQVQVQSGAEVKKPGSSSVKYSCKASGYFTDTAIQWVQAP 60
QY 61 GGGLEWIGVINIYDNNYNOKFKGKATMTVDKSTAYWELSLRSEDPAVYVCAR-- 117
DB 61 GGGLEWIGVINIYDNNYNOKFKGKATMTVDKSTAYWELSLRSEDPAVYVCAR-- 117
QY 118 -AAMYDYWGCGTLTVSS 135
DB 121 TGSSEYFDYWGCGTLTVSS 139

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ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=81234548; PubMed=6788376;
RX Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00539; AAA38172.1; -.
DR PIR; A02038; GMS43.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 54 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 67.8%; Score 488; DB 1; Length 137;
Best Local Similarity 67.2%; Pred. No. 6e-42;
Matches 92; Conservative 15; Mismatches 28; Indels 2; Gaps 1;

QY 1 MGNACITFLVTTATGVSQVQVQSGAEVKKPGSSSVKYSCKASGYFTDTAIQWVQAP 60
DB 1 MGNWCMFLFAATATGVSQVQVQSGAEVKKPGSSSVKYSCKASGYFTDTAIQWVQAP 60
QY 61 GGGLEWIGVINIYDNNYNOKFKGKATMTVDKSTAYWELSLRSEDPAVYVCAR--RA 118
DB 61 GGGLEWIGVINIYDNNYNOKFKGKATMTVDKSTAYWELSLRSEDPAVYVCAR--RA 118
QY 119 AAMYDYWGCGTLTVSS 135
DB 121 GRYDYWGCGTLTVSS 137

```

RESULT 3  
HV11\_MOUSE

RESULT 4  
HV48\_MOUSE  
ID HV48\_MOUSE STANDARD; PRT; 138 AA.  
AC P03980;  
DT 23-OCT-1986 (Rel. 02, Created)  
DT 23-OCT-1986 (Rel. 02, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)



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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00493; AAA38128.1; -.
DR PIR: A02028; HVMWG7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBEB31DA5CE8 CRC64;

Query Match 67.2%; Score 483.5; DB 1; Length 140;
Best Local Similarity 65.7%; Pred. No. 1.7e-41;
Matches 92; Conservative 17; Mismatches 26; Indels 5; Gaps 1;

QY 1 MGWNCIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDVAIQWVQAP 60
Dd 1 MGWSPFLFLSVTGVAGVHSEVQLQDSGAEIVAGSSVKMSCKASGYTFTSYGINVVKQP 60
QY 61 GQGLEWICVNIYIDNTNYNQKFKKATMYDYSKISTAYMELSSRSEPTAYYCARAAW 120
Dd 61 GQGLEWICVINYGNQYINYNKFKKTLTYDQSSSTAYMOLRSITSEDSAYVFCARSHY 120
QY 121 Y-----MDYWGQGLVTVSS 135
Dd 121 YGGSYDFPYWGQGLTVTVSS 140

RESULT 6
ID HY06_MOUSE STANDARD: PRT: 117 AA.
HY06_MOUSE
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_Taxid=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCLETAEDOS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: A02032; HVM502.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DISULFID 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DDB51FCAB8 CRC64;

Query Match 65.3%; Score 470; DB 1; Length 117;

```

Best Local Similarity 76.7%; Pred. No. 3,1e-40;  
Matches 89; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

OY 1 MGNMCIIFLVATATGVSQVQLVQSGAEVKKPPSSVKVSCSKASGYFTFDTAIGWVQAP 60  
DB 1 MGNMCIIFLVATATGVSQVQLVQSGAEVKKPPSSVKVSCSKASGYFTFDTAIGWVQAP 60  
OY 61 GGGLEWIGVINIYDNTNNOKEFGKATMTVDKSTAYMELSLRSEDPAVYYCAR 116  
DB 61 GGGLEWIGRIHPSDDTNNQKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYYCA 116

## RESULT 7

HV03\_MOUSE STANDARD; PRT; 117 AA.

AC P01749;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE IG HEAVY CHAIN V REGION 3 PRECURSOR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NpB family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).

CC -I- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY  
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; J00536; AAA38605.1; -  
DR PIR; A02031; HVMS3.  
DR InterPro; IPR003006; -  
DR Pfam; PF00047; 1g; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.  
FT DOMAIN 20 49 FRAMEWORK 1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 55 68 FRAMEWORK 2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 86 117 FRAMEWORK 3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

Query Match 64.3%; Score 463; DB 1; Length 117;  
Best Local Similarity 75.6%; Pred. No. 1,6e-39;  
Matches 90; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

OY 1 MGNMCIIFLVATATGVSQVQLVQSGAEVKKPPSSVKVSCSKASGYFTFDTAIGWVQAP 60  
DB 1 MGNMCIIFLVATATGVSQVQLVQSGAEVKKPPSSVKVSCSKASGYFTFDTAIGWVQAP 60  
OY 61 GGGLEWIGVINIYDNTNNOKEFGKATMTVDKSTAYMELSLRSEDPAVYYCAR 117  
DB 61 GGGLEWIG--NIYPSDSETHYNOKFKDKATLTVDKSSSTAYMQLSLTSEDSAVYYCAR 117

RESULT 8  
HV04\_MOUSE STANDARD; PRT; 117 AA.

AC P01748;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE IG HEAVY CHAIN V REGION 23 PRECURSOR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NpB family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).

CC -I- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY  
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
CC -----  
DR PIR; A02030; HVMS23.  
DR InterPro; IPR003006; -  
DR Pfam; PF00047; 1g; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.  
FT DOMAIN 20 49 FRAMEWORK 1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 55 68 FRAMEWORK 2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 86 117 FRAMEWORK 3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F9B CRC64;

Query Match 62.1%; Score 447; DB 1; Length 117;  
Best Local Similarity 71.8%; Pred. No. 6,2e-38;  
Matches 84; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

OY 1 MGNMCIIFLVATATGVSQVQLVQSGAEVKKPPSSVKVSCSKASGYFTFDTAIGWVQAP 60  
DB 1 MGNMCIIFLVAAANGVSHQVQLVQSGAEVKKPPSSVKVSCSKASGYFTFDTAIGWVQAP 60  
OY 61 GGGLEWIGVINIYDNTNNOKEFGKATMTVDKSTAYMELSLRSEDPAVYYCAR 117  
DB 61 GGGLEWIGINIPGNGTNNYNEKFSKVTLTVDKSSSTAYTQLSLTSEDSAVYYCAR 117

## RESULT 9

HV1B\_HUMAN STANDARD; PRT; 117 AA.

AC P01743;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE IG HEAVY CHAIN V-1 REGION H63 PRECURSOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=83144028; PubMed=6298778;  
RA Rechevali G., Ram D., Glazer L., Zakut R., Givol D.;  
RT "Evolutionary aspects of immunoglobulin heavy chain variable region  
RT (VH) gene subgroups.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).

CC -----



ID	HV49_MOUSE	STANDARD:	PRT:	117 AA.		
AD	E23083;					
DT	01-NOV-1991 (Rel. 20, Created)					
DT	01-NOV-1991 (Rel. 20, Last sequence update)					
DT	15-JUL-1999 (Rel. 38, Last annotation update)					
DE	IG HEAVY CHAIN V-I REGION V35 PRECURSOR.					
OS	Homo sapiens (Human).					
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OX	NCBI_Taxid=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=86296408; PubMed=2841108;					
RA	Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,					
RA	Ohno H., Fukuhara S., Honjo T.;					
RT	"Dispersed localization of D segments in the human immunoglobulin					
RL	heavy-chain locus."					
RL	EMBO J. 7:1047-1051(1988).					
CC	-----					
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/					
CC	or send an email to license@isb-sib.ch).					
CC	-----					
DR	EMBL; X07448; ? NOT_ANNOTATED_CDS.					
DR	PIR; S00476; HVH035.					
DR	InterPro: IPR003006; -					
DR	Pfam; PF00047; 19; 1.					
KW	Immunoglobulin V region; Signal.					
FT	SIGNAL	1	19			
FT	CHAIN	20	117	IG HEAVY CHAIN V-I REGION V35.		
FT	NON_TER	117	117			
SO	SEQUENCE	117 AA;	13009 MW;	B61CE63F8CE97BD CXC64;		
QY	Query Match	61.0%;	Score 439;	DB 1; Length 117;		
	Best Local Similarity	73.5%;	Pred. No. 3.9e-37;			
	Matches	86; Conservative	6; Mismatches	25; Indels	0; Gaps	0;
Dy	1	MGNNCTIFFLVLTATGAGSVOVLQSGAEVKKPPGSSVSCASGYETPDVAIQWRQAP	60			
Dy	1	MDWTIRFLFVAALGAHSOVLQSGAEGKPGASVAVSCASYTFGTGMHWVRAP	60			
OY	61	GCGLEWICVINIYYDNTNYNOKFKAKATMYDKSTSTAYMELSLRSEPTAYVCAR	117			
Dy	61	GCGLEWMGRINPNSGTYNAQKFGCRVYSTRTISTAYMELSLRSDPTVYYVCAR	117			
RESULT	13					
HV49_MOUSE	STANDARD:	PRT:	117 AA.			
AC	P06328;					
DT	01-JAN-1988 (Rel. 06, Created)					
DT	01-JAN-1988 (Rel. 06, Last sequence update)					
DT	15-JUL-1999 (Rel. 38, Last annotation update)					
DE	IG HEAVY CHAIN V REGION VH58 B4 PRECURSOR.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_Taxid=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=85099340; PubMed=2578321;					
RA	Yancopoulos G.D., Alt F.W.;					
RT	"Developmentally controlled and tissue-specific expression of					
RL	unrearranged VH gene segments."					
RL	Cell 40:271-281(1985).					
CC	-----					
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CC	
CC	EMBL: M13788; AAA38506.1; --
DR	PIR: A02035; MEMSB4.1
DR	InterPro: IPR003006; .
DR	Pfam: PF00047; 1g; 1.
RW	Immunoglobulin V region; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT	DOMAIN 20 49 FRAMEWORK 1.
FT	DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 55 68 FRAMEWORK 2.
FT	DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 86 117 FRAMEWORK 3.
FT	DISULFID 41 115 BY SIMILARITY.
FT	NON_TER 117 117
SO	SEQUENCE 117 AA; 12834 MW; B8862PACG7ABD345 CRC64;
<hr/>	
Qy	Query Match 60.4%; Score 435; DB 1; Length 117; Best Local Similarity 69.2%; Pred. No. 9.7e-37;
Dd	Matches 81; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
Oy	1 MGWNIIIFELVATTAAGHSOVOLYOSGAEVRKPGSSVVCASCASGYTFDAIOWRPAP 60           :   1 MGVSMIMFLAATAGVSHSPVLQDPGLAEKPGGSVALSKCASGYITFTSWHMYVKORP 60
Dd	61 GGGLEMGIVGINYYDNTVYNOKFKGRATMTTVDKSTSTRAMELSLRSBDTAVYYCAR 117   :           :   61 GNGLEWMIGNIDPNSCGTYNKKERKSKATLYDKPSSTAYMQLSLSBDSNAVYYCTR 117
<hr/>	
RESULT 14	
HV10_MOUSE	STANDARD: PRT; 117 AA.
ID	HV10_MOUSE
AC	P01754; P11270;
DT	21-JUL-1986 (Rel. 01, Created)
DT	01-JUL-1989 (Rel. 11, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG HEAVY CHAIN V REGION 145 PRECURSOR.
OS	Mus musculus (Mouse);
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6;
RX	MEDLINE=81234548; PubMed=6788376;
RA	Bochwell A.L.M., Paakind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
RL	"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
RT	Cell 24:625-637(1981)..
CC	-I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC	
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CC	
DR	EMBL: J00533; AAA38602.1; --
DR	PIR: C02034; HYMS45;
DR	InterPro: IPR003006; --
DR	Pfam: PF00047; 1g; 1.
RW	Immunoglobulin V region; Signal.





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OM protein - protein search, using sw model

Run on: April 25, 2001, 09:37:15 ; Search time 39.12 Seconds  
(without alignments)  
404.475 Million cell updates/sec

Title: US-09-249-011-6  
Perfect score: 720  
Sequence: 1 MGNWCIIFLVTATGVSQ.....ARAWMDYWGQGLTVSS 135

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_15:  
2: sp\_archaea:  
3: sp\_bacteria:  
4: sp\_fungi:  
5: sp\_human:  
6: sp\_invertebrate:  
7: sp\_mhc:  
8: sp\_mammal:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_protent:  
12: sp\_unclassified:  
13: sp\_vertebrate:  
14: sp\_virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	454	63.1	124	4 Q9UL92	Q9UL92 homo sapien
2	441.5	61.3	119	4 Q9UL94	Q9UL94 homo sapien
3	437	60.7	116	4 Q9UL89	Q9UL89 homo sapien
4	436.5	60.6	117	11 Q9QX89	Q9QX89 mus musculu
5	432.5	60.1	150	4 Q9Y298	Q9Y298 homo sapien
6	429.5	59.7	117	11 Q9QX80	Q9QX80 mus musculu
7	423	58.8	109	11 Q9JL75	Q9JL75 mus musculu
8	422.5	58.7	125	4 Q9UL95	Q9UL95 homo sapien
9	415.5	57.7	157	4 Q9S978	Q9S978 mus musculu
10	411	57.1	118	11 Q9Z1C4	Q9Z1C4 mus musculu
11	383	53.2	114	11 Q9JL81	Q9JL81 mus musculu
12	382	53.1	110	11 Q9JL77	Q9JL77 mus musculu
13	366.5	50.9	117	11 Q9Z1C6	Q9Z1C6 mus musculu
14	357	49.6	110	11 Q9JL83	Q9JL83 mus musculu
15	343.5	47.7	113	4 Q9UL90	Q9UL90 homo sapien
16	341.5	47.4	116	4 Q9UL93	Q9UL93 homo sapien
17	335	46.5	147	4 Q9Y509	Q9Y509 homo sapien
18	333	46.2	298	11 Q9QYF0	Q9QYF0 mus musculu
19	332.5	46.2	109	11 Q9JL85	Q9JL85 mus musculu

20	322	44.7	122	4 Q9UL84	Q9UL84 homo sapien
21	320	44.4	118	4 Q9UL91	Q9UL91 homo sapien
22	317.5	44.1	121	4 Q9UL71	Q9UL71 homo sapien
23	312.5	43.4	131	4 Q9UL88	Q9UL88 homo sapien
24	307.5	42.7	102	11 Q9JL79	Q9JL79 mus musculu
25	298.5	41.5	119	4 Q9UL73	Q9UL73 homo sapien
26	298	41.4	124	6 Q9N0W4	Q9N0W4 oryctolagus
27	297	41.2	118	4 Q9UL72	Q9UL72 homo sapien
28	295	41.0	124	6 Q9N0W6	Q9N0W6 oryctolagus
29	294	40.8	437	11 Q9R1A4	Q9R1A4 mus musculu
30	280.5	39.0	112	4 Q9UGP3	Q9UGP3 homo sapien
31	279.5	38.8	104	4 Q9UL87	Q9UL87 homo sapien
32	257	35.7	150	4 Q9S973	Q9S973 homo sapien
33	252	35.0	95	4 Q9UL86	Q9UL86 homo sapien
34	246	34.2	122	4 Q9UL75	Q9UL75 homo sapien
35	234.5	32.6	121	4 Q9UL96	Q9UL96 homo sapien
36	209.5	29.1	82	4 Q9NP6	Q9NP6 homo sapien
37	205	28.5	416	4 Q9NP6	Q9NP6 homo sapien
38	204.5	28.4	76	4 Q9S742	Q9S742 homo sapien
39	193.5	26.9	82	4 Q9S725	Q9S725 homo sapien
40	192	26.7	77	4 Q9S726	Q9S726 homo sapien
41	191.5	26.6	88	4 Q9S737	Q9S737 homo sapien
42	191	26.5	80	4 Q9S727	Q9S727 homo sapien
43	189.5	26.3	118	4 Q9UL74	Q9UL74 homo sapien
44	188	26.1	77	4 Q9S728	Q9S728 homo sapien
45	187.5	26.0	79	4 Q9S731	Q9S731 homo sapien

## ALIGNMENTS

RESULT 1  
Q9UL92 PRELIMINARY; PRT; 124 AA.  
AC Q9UL92;  
DT 01-MAY-2000 (TRENBLREL. 13, Created)  
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)  
DT 01-JUN-2000 (TRENBLREL. 14, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035022; AAD56258.1; -;  
DR INTERPRO; IPR003006; -;  
DR PFM; PF00047; 1g; 1.  
FT NON\_TER 1 124  
FT NON\_TER 1 124  
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 63.1%; Score 454; DB 4; Length 124;  
Best Local Similarity 71.0%; Pred. No. 2.9e+40;  
Matches 88; Conservative 13; Mismatches 15; Indels 8; Gaps 1;

QY 20 QVALVSGAEVKKPGSSVSKASGYFTTDYAIQWROAPGQGLWGVNIYDNTNY 79  
DB 1 EVOLVESGAEEVKKPGASVSKASGYFTTAYYCAHAWM-----HYMGQGTIV 60  
QY 80 NQKFGKATWYDKSRSTAYVMSLSRSDTAYYCAHAWM-----HYMGQGTIV 131  
DB 61 AAKFGGRVMTDSTSTVYMLSSLRSDTAYYCARGLVVPAAVSRRFDYMGQGTIV 120  
QY 132 TVSS 135  
|||||

Db 121 TVSS 124

## RESULT 2

ID 09UL94 PRELIMINARY; PRT: 119 AA.

AC 09UL94;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RT Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL EMBL: AF035020; AAD56256.1; -.

DR INTERPRO: IPR003006; -.

PFAM: PF00047; 19; 1.

FT NON\_TER 1 1

FT NON\_TER 119 119

SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345FA16E CRC64;

Query Match 61.3%; Score 441.5; DB 4; Length 119;

Best Local Similarity 74.2%; Pred. No. 5.7e-39;

Matches 89; Conservative 8; Mismatches 18; Indels 5; Gaps 2;

QY 20 QVQLVSGAEVKKRQSSVKVSKASGTFPTDYAIQWVROAPGQGLEWIGYINITYDNTNY 79

DB 1 EVQLVSGAEVKKRQSSVKVSKASGTFPTGYVHWVROAPGQGLEWGMINPMSMTNY 60

QY 80 NQKFKATMTVDKSTSTAVMELSLRSEDPYAVYCARAA---WYDYGQGLTVYSS 135

DB 61 AQRFGKAVTMTKDTISITATMELSLRSDPTAVYTCARGGGRLMF-DPMGQGLTVYSS 119

## RESULT 3

ID 09UL89 PRELIMINARY; PRT: 116 AA.

AC 09UL89;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RT Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL EMBL: AF035025; AAD56261.1; -.

DR INTERPRO: IPR003006; -.

PFAM: PF00047; 19; 1.

FT NON\_TER 1 1

FT NON\_TER 116 116

SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EAB98 CRC64;

Query Match 60.7%; Score 437; DB 4; Length 116;

Best Local Similarity 75.0%; Pred. No. 1.6e-38;

Matches 87; Conservative 7; Mismatches 18; Indels 4; Gaps 1;

QY 24 VQSGAEVKKRQSSVKVSKASGTFPTDYAIQWVROAPGQGLEWIGYINITYDNTNYQKF 83

DB 1 VQSGAEVKKRQSSVKVSKASGTFPTDYAIQWVROAPGQGLEWIGYINITYDNTNYQKF 60

QY 84 KGKATMTVDKSTSTAVMELSLRSEDPYAVYCARAA---WYDYGQGLTVYSS 135

DB 61 QGRFTITADNSTSTAVMELSLRSEDPYAVYCARAA---WYDYGQGLTVYSS 116

## RESULT 4

ID 09OXE9 PRELIMINARY; PRT: 117 AA.

AC 09OXE9;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX Clemens A., Rademakers A., Specht C., Koelsch E.;

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ225174; CAB65237.1; -.

DR INTERPRO: IPR003006; -.

PFAM: PF00047; 19; 1.

FT NON\_TER 1 1

FT NON\_TER 117 117

SQ SEQUENCE 117 AA; 13000 MW; CDDEZAF84D99734 CRC64;

Query Match 60.6%; Score 436.5; DB 11; Length 117;

Best Local Similarity 71.8%; Pred. No. 1.9e-38;

Matches 84; Conservative 16; Mismatches 16; Indels 1; Gaps 1;

QY 20 QVQLVSGAEVKKRQSSVKVSKASGTFPTDYAIQWVROAPGQGLEWIGYINITYDNTNY 79

DB 1 EVQLVSGAEVKKRQSSVKVSKASGTFPTDYVKKVQSGHSLWIGINPNNGTSTY 60

QY 80 NQKFKATMTVDKSTSTAVMELSLRSEDPYAVYCARAAW---WDYDYGQGLTVYSS 135

DB 61 NQKFKATMTVDKSSSTAVMELSLRSEDPYAVYCARAAW---WDYDYGQGLTVYSS 117

## RESULT 5

ID 09Y298 PRELIMINARY; PRT: 150 AA.

AC 09Y298;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE IGG VH PROTEIN PRECURSOR (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98322155; PubMed=9657749;

RA Jacquemin M.G., Vander Elst L.P.L.;

RT "Mechanism and kinetics of factor VII inactivation: study with an

RT IgG4 monoclonal antibody derived from a hemophiliat A patient with an

RT inhibitor.";

RL Blood 92:496-506(1998)

DR EMBL: AJ224083; CAI1829.1; -.

DR INTERPRO: IPR003006; -.

DR PFAM: PF00047; 19; 1.



KW Signal. 1 19 POTENTIAL.  
FT SIGNAL. 150 150  
SQ SEQUENCE 150 AA: 16031 MW: 563D164AB22802D5 CRC64:

Query Match  
Best Local Similarity 60.1%; Score 432.5; DB 4; Length 150;  
Matches 86; Conservative 13; Mismatches 36; Indels 1; Gaps 1;

OY 1 MGNWCIIFLVTTATGVSQVQVLOSAGAEVKKRPGSSVSKVSCASGYTFTDYAIOQVWQAP 60  
DB 1 MDWTRILFLVAAATGTHAOVOLVOSAGAEVKKRPGASVSKVSCGYTTLTLPVHWGAP 60  
OY 61 GGGLEWIGVINYDNTNYNOKFKATVTVDKSTSTAMELSSLRSEPTAVYYCA-RAA 119  
DB 61 GGGLEWVSFDESGESSTIYAREFGQSVTMTADTSTDIAYMELSSLRSDTAVYYCAVPDP 120  
OY 120 WYMDYMGOGTLVTSS 135  
DB 121 DAFDIMGCTMTVTSS 136

RESULT 6  
O90XF0 PRELIMINARY: PRT: 117 AA.

AC O90XF0.  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Clemens A., Rademakers A., Specht C., Koelsch E.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ225171; CAB5236.1; .  
DR INTERPRO: IPR003006; .  
DR PFM: PF00047; 19; 1.  
FT NON\_TER 1 1  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA: 13060 MW: D816AD0858A47E4C CRC64:

Query Match  
Best Local Similarity 59.7%; Score 429.5; DB 11; Length 117;  
Matches 82; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

OY 20 QOVQVSGAEVKKPGSSVSKVSCASGYTFTDYAIOQVWQAPGQGLEWIGVINYDNTNY 79  
DB 1 EVOVLQOOSGELVKKPGASVSKVSCASGYTFTDYMKVWKSHKSLLEWIDINDPNNNGTISY 60  
OY 80 NOKFKKATMTYDKSTSTAYMELSSLRSEDTAVYYCAR-AAAYMDYMGOGTLVTSS 135  
DB 61 NOKFKKATLTVDKSSSTAYMQLNLSLSDSAVYYCARDKDYFDYMGOGTLVTSS 117

RESULT 7  
O9JL75 PRELIMINARY: PRT: 109 AA.  
AC O9JL75.  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/C.  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-  
acetyl-glucoamine antibodies from mice with autoimmune myocarditis."  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF206031; AAF69329.1; .  
FT NON\_TER 1 1  
FT NON\_TER 109 109  
SQ SEQUENCE 109 AA: 12118 MW: FF65E441BBF936A6 CRC64:

Query Match  
Best Local Similarity 58.8%; Score 423; DB 11; Length 109;  
Matches 80; Conservative 10; Mismatches 17; Indels 2; Gaps 1;

OY 29 EVKPKSSVSKVSCASGYTFTDYAIOQVWQAPGQGLEWIGVINYDNTNMQKFKAT 88  
DB 1 ELVKKPGASVSKVSCASGYTFTSYVMHWKQKPGQGLEWIGVINYDNTKYNKFKAT 60  
OY 89 MTVDKSTSTAYMELSSLRSEDTAVYYCARAWY--MDYMGOGTLVTSS 135  
DB 61 LPSDKSSSTAYMELSLTSEDSAVYYCARQGNVGFYMGOGTLVTSS 109

RESULT 8  
O9UL95 PRELIMINARY: PRT: 125 AA.

AC O9UL95.  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-98277139; PubMed-9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL: AF035019; AAD56255.1; .  
DR INTERPRO: IPR003006; .  
DR PFM: PF00047; 19; 1.  
FT NON\_TER 1 1  
FT NON\_TER 125 125  
SQ SEQUENCE 125 AA: 13516 MW: 0D3CD5C232488EAC CRC64:

Query Match  
Best Local Similarity 58.7%; Score 422.5; DB 4; Length 125;  
Matches 85; Conservative 10; Mismatches 21; Indels 9; Gaps 1;

OY 20 QOVQVSGAEVKKPGSSVSKVSCASGYTFTDYAIOQVWQAPGQGLEWIGVINYDNTNY 79  
DB 1 EVOVLVSGAEVKKPGASVSKVSCASGYTFTGYMHWVWQAPGQGLEWIMGINDPNSGTYN 60  
OY 80 NOKFKKATMTYDKSTSTAYMELSSLRSEDTAVYYCAR-----AAAYMDYMGOGTL 130  
DB 61 AOKVQGRVTMTDTTISTAYMELSLRLSDTAVYYCARSGGRIAAADAFDIMGGT 120  
OY 131 VTSS 135  
DB 121 VTSS 125

RESULT 9  
O9S978 PRELIMINARY: PRT: 157 AA.



FT	NON_TER	1	1	
FT	NON_TER	110	110	
SQ	SEQUENCE	110 AA;	12138 MW;	2EDE81FB5862C9AF CRC64;

Query Match	53.1%	Score 382;	DB 11;	Length 110;
Best Local Similarity	68.9%;	Pred. No. 9.1e-33;		
Matches 73; Conservative	14;	Mismatches 17;	Indels 2;	Gaps 1;

Qy	32	KPGSGVWVSCKASGYFTTUAIAQWRAAGGGLLEIGVILNYLQNTYCNVNRKFGKATITLV	91
		:     :     :     :     :     :     :     :     :     :     :     :	
Db	5	RPGASVYKLSCKASGYFTFSMMNHMAKQIRGCGGLEIGLISLHNSGHTITVNEKRFKATITLV	644
Qy	92	DKSTIATMELSLKSEDTAAVYTCARAA--WTMDWGQGLVTYVSS	135
		:     :     :     :     :     :     :     :     :     :     :	
Db	65	DTSSSTAYVLDLSLTSEDSAAVYTCARQRNRYAMDYWGQGTVTYVSS	110

RESULT 13  
Q921C6

DT	01-MAY-1999	(TREMBLrel. 10, Created)	
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)	
DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)	
DE	ANTI-FORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).		
OS	Mus musculus (mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BALB/C;		
RA	Mueller J.P., Gannon M.A., Hartman S.L., Elliott E.A., Squinto S.P.,		
RA	Matis L.M., Evans M.U.;		
RT	"Humanized porcine VCAM-specific monoclonal antibodies with chimeric		
RT	1992/64 constant regions block human leukocyte binding to porcine		
RT	endothelial cells."		
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: U78799; AAD00291.1; -.		
DR	INTERPRO: IPR003006; -.		
DR	PFAM: PF00047; 1g; 1.		
FT	NON_TER	1	
FT	NON_TER	117	1
Q0	SEQUENCE	117 AA; 13122 MW; 4F65B193AFB77E5B CRC64;	

Query Match	50.98;	Score 366.5;	DB 11;	Length 117;
Best Local Similarity	59.38;	Pred. No. 4.1e-31;		
Matches 70; Conservative	19;	Mismatches 26;	Indels 3;	Gaps 2

QY 0VQLVSGAVKRRGSSSVYSCASPTTDDAIOWAQAAGGGLEMTIGVINYIDNTN 75  
 ||| ||| : : : ||| ||| ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| |||  
 Db 1 QVQLDQSGLYARPGISVAISCASYSSTSYMMHWNAQRGGDLMTGMIDPSDSYLK 60  
 QY 80 NQRFKAINTVDKSTSIAMELSLRSEDPAIVYCARR--AAAMYDWGGCLTVASS 135  
 ||| ||| : : : ||| ||| ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| |||  
 Db 61 NORLKDAILITDKSNTLTAMWFGSDTSNVSAVVCTGTGEVSMA--TWGGCLTVYSA 117

RESULT	14
09JL83	
ID	09JL83
AC	09JL83;
DT	01-OCT-2000 (TREMBLrel. 15, created)
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE	ANTI-WYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
OS	Mus musculus (mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX	NCB1-TaxID=10090;
NN	[1]

RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/C;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "Characterization of cross-reactive monoclonal anti-mysin/anti-n-  
acetyl-glucosamine antibodies from mice with autoimmune myocarditis."  
RL submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF206023; AAF69321.1; -  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match	49.6%;	Score 357;	DB 11;	Length 110;
Best Local Similarity	-64.2%;	Pred. NO. 3.8e-30;		
Matches	70;	Conservative 15;	Mismatches 22;	Indels 2;
				Gaps 1;

Oy	29	EKKPSSSVKSCASGAYETFDYALIAWQAOAGGLEIMIGVINYLYNTYNYNOKRFGKAT	88
		:	
Dd	2	ELVPFGSAVISCASGYIFFNSMMNMWYLRCGGCLEMIGTITCGDDGDAYTNCKRFPGKAT	61
Oy	89	MIVDKSTSTAMELSSLRESDIYAVYYCARAA--MDYWGGCTLVTVSS	135
		:	
Dd	62	LTKAKSSTAIYQLSLTSVDASYEFCAASNDVDEAFATWGGLTVTVSA	110

RESULT	15	
09UL90		
ID	09UL90	PRELIMINARY;
09UL90		PRT; 113 AA

DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)  
DT 01-JUN-2000 (TREMblrel. 14, last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RT Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035024; AAD56260.1; -.  
DR INTERPRO; IPR003006; -.  
DR PFAM; PF00047; 1g; 1.  
ET NON\_TER 1 1  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match	47.7%;	Score 343.5;	DB 4;	Length 113;
Best Local Similarity	55.1%;	Pred. No. 1e-26;		
Matches	65;	Conservative	24;	Mismatches 22;
				Indels 7;
				Gaps 3;

Qy 20 QYVLVSGAGVKKRPGSSVWVSCASGYPTTDDA IOWRQAQGGLEMTGVNITLYDNTN - 78  
 Db 1 EVOLVESGGGVDPGGSRLRSCASGFTTSSGMMHWQAQKGLENVAFLR -- YDGSNK 55  
 Qy 79 -YNQFKGATWTVDKSTSTAIWELSSLESDTAVVYCYARAPAMDYWGQGLTYVSS 135  
 Db 59 YYADSVAGRPTLIRDSKNLTLYIQNNLSLAEDTAAVYCYAKR - LNWYGGQGLTYVSS 113

Search completed: April 25, 2001, 09:40:33  
Job time: 198 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2001, 09:36:42 ; Search time 36.24 Seconds  
(without alignments)  
212.943 Million cell updates/sec

Title: US-09-249-011-6  
Perfect score: 720  
Sequence: 1 MGNMCIFFLVTTATGVHSQ.....ARAWMYDYGCGCLVTSS 135

Scoring table:  
BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues  
Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
A.GeneSeq\_0401.\*  
1: /SIDSL/gcgdata/geneseq/geneseqp/AA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseqp/AA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseqp/AA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseqp/AA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseqp/AA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseqp/AA1985.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseqp/AA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseqp/AA1987.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseqp/AA1988.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseqp/AA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseqp/AA1990.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseqp/AA1991.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseqp/AA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseqp/AA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseqp/AA1994.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseqp/AA1995.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseqp/AA1996.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseqp/AA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseqp/AA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseqp/AA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseqp/AA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseqp/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720	100.0	135	21	B07965 A heavy chain vari
2	627	87.1	135	21	B07963 Amino acid sequenc
3	585.5	81.3	470	21	W90935 Humanised anti-Fas
4	582.5	80.9	470	21	W90933 Humanised anti-Fas
5	581.5	80.8	470	21	W90934 Humanised anti-Fas
6	579.5	80.5	470	19	W83037 Anti-Fas humanised
7	579.5	80.5	470	21	B14779 Humanised anti-Fas
8	579.5	80.5	470	21	W90929 Humanised HFE7A de
9	573.5	79.7	140	15	R55556 DRG-200 Humanized
10	567.5	78.8	470	21	W90936 Humanised HFE7A de
11	566.5	78.7	145	19	W83038 Anti-Fas humanised

12	566.5	78.7	145	21	B14775	Fragment of human
13	566.5	78.7	145	21	W90925	Humanised anti-Fas
14	566.5	78.7	470	19	W83036	Anti-Fas humanised
15	566.5	78.7	470	21	B14776	Humanised anti-Fas
16	566.5	78.7	470	21	W90926	Humanised HFE7A de
17	554	76.9	588	19	W71880	Anti-human Fas hum
18	554	76.9	588	19	B12917	Anti-human Fas hum
19	546	75.8	135	13	R24107	Humanised anti-Fas
20	545	75.7	135	11	R06369	Humanised anti-Fas
21	540	75.0	135	21	Y80289	Anti-Fas heavy cha
22	537	74.6	135	21	Y80288	Humanised anti-Fas
23	532	73.9	588	19	W71881	Anti-human Fas hum
24	532	73.9	588	21	B12918	Anti-human Fas hum
25	531.5	73.8	163	12	R15060	Murine anti-Fas m
26	531.5	73.8	163	12	R15200	Anti-human Fas imm
27	530.5	73.7	136	21	Y77596	Anti-human VEGF re
28	530.5	73.7	140	18	W21847	Humanised heavy ch
29	530	73.6	135	21	Y80291	Humanised anti-Fas
30	530	73.6	468	13	R28808	pre-5A8 humanised
31	529.5	73.5	136	15	R59512	Sequence of the he
32	529	73.5	133	16	R81840	F-selectin CDR-gra
33	529	73.5	139	19	W36165	Humanised heavy ch
34	528.5	73.4	464	19	W83041	Anti-Fas Mab HFE7A
35	528.5	73.4	464	21	B14747	Mouse anti-Fas ant
36	528.5	73.4	464	21	W90897	Murine anti-Fas an
37	528	73.3	137	21	Y99847	Humanised partial
38	527	73.2	135	13	R29017	pIC-Rh-1220d. Sy
39	527	73.2	139	19	W65773	Anti-human HML.24
40	527	73.2	139	19	W62205	Humanised anti-HML
41	527	73.2	139	20	Y32770	Anti-HML.24 antibo
42	527	73.2	139	20	Y02572	Humanised H chain
43	527	73.2	139	20	Y05486	H chain V region o
44	527	73.2	140	19	W77294	HML.24 antibody he
45	526	73.1	135	13	R29016	pIC-Rh-1220b. Sy

## ALIGNMENTS

RESULT 1	
ID B07965	standard; Protein: 135 AA.
AC B07965;	
XX	
DT 14-NOV-2000	(first entry)
XX	
DE	A heavy chain variable region of humanised 3S1 antibody.
XX	
KW	Antibody 301; B7 molecule; B7; humanised immunoglobulin;
KW	autoimmune disease; infectious disease; inflammatory disorder;
KW	systemic lupus erythematosus; diabetes mellitus; insulin; asthma;
KW	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW	multiple sclerosis; transplant rejection; proliferative disease;
KW	leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW	aplastic anaemia; myeloid dysplasia syndrome.
XX	
OS	Synthetic.
OS	Mus sp.
OS	Homo sapiens.
XX	
FT	Key
FT	Peptide
FT	1..19
FT	/note= "signal peptide"
FT	20..135
FT	/note= "mature protein"
FT	50..54
FT	/note= "complementarity determining region 1"
FT	69..85
FT	/note= "complementarity determining region 2"
FT	118..124
FT	/note= "complementarity determining region 3"
XX	

PN W0200047625-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PE 09-FEB-2000: 2000M0-US03303.  
 XX  
 PR 12-FEB-1999: 990S-0249011.  
 PR 24-JUN-1999: 990S-0339596.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX  
 DR WPI: 2000-524532/47.  
 DR N-PSDB: A59694.  
 XX  
 PT Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 PS Example 3; Fig 2A; 162pp; English.  
 XX  
 CC The present sequence represents the heavy chain variable region  
 CC of the humanised murine antibody 3D1. The antibody has a binding  
 CC specificity to B7 molecules. The antibody is used to construct humanized  
 CC immunoglobulins, which comprise an antigen binding region of non-human  
 CC origin and a portion of a human immunoglobulin. The humanized  
 CC immunoglobulins are useful for treating autoimmune diseases, infectious  
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 CC  
 XX  
 SQ Sequence 135 AA;  
 XX  
 QY 1 MGNWCIIFLVTATGVSQVQLVQSGAEVKKPSSSVKSCASGYPTDVAIQMWRQAP 60  
 Db 1 mgwncilflvtatgvsqqlvqsgaevkkpsssvkscasgyftdyaiqwrqap 60  
 QY 61 GGGLEWIGVINIYDNTNYNQKFKGKATMVDKSTAYMELSLRSEDVAVYCARAAW 120  
 Db 61 ggglewigvinilydntnynqgkfkgaatmvdksctaymelslrsedtavycaraaw 120  
 QY 121 YMDYWGOGTLVTSS 135  
 Db 121 ymdywgogtlvtvss 135  
 XX  
 RESULT 2  
 B07963  
 ID B07963 standard: Protein: 135 AA.  
 XX  
 AC B07963;  
 XX  
 DT 14-NOV-2000 (first entry)  
 XX  
 DE Amino acid sequence of heavy chain variable region of 3S1 antibody.  
 XX  
 XX Antibody 3D1: B7 molecule; B7: humanised immunoglobulin;  
 KW autoimmune disease; infectious disease; inflammatory disorder;  
 KW systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;  
 KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;

KW multiple sclerosis; transplant rejection; proliferative disease;  
 KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;  
 KW aplastic anaemia; myeloid dysplasia syndrome.  
 XX  
 OS Mus sp.  
 XX  
 XX Key  
 FH Peptide  
 FT 1..19  
 FT /note- "signal peptide"  
 FT 20..135  
 FT Protein  
 FT /note- "mature protein"  
 FT 50..54  
 FT /note- "complementarity determining region 1"  
 FT 69..85  
 FT /note- "complementarity determining region 2"  
 FT 118..124  
 FT /note- "complementarity determining region 3"  
 XX  
 XX W0200047625-A2.  
 XX  
 XX 17-AUG-2000.  
 XX  
 PE 09-FEB-2000: 2000M0-US03303.  
 XX  
 PR 12-FEB-1999: 990S-0249011.  
 PR 24-JUN-1999: 990S-0339596.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX  
 DR WPI: 2000-524532/47.  
 DR N-PSDB: A59692.  
 XX  
 PT Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 PS Example 1; Fig 1A; 162pp; English.  
 XX  
 CC The present sequence represents the heavy chain variable region of the  
 CC murine antibody 3D1. The antibody has a binding specificity to B7  
 CC molecules. The antibody is used to construct humanized immunoglobulins,  
 CC which comprise an antigen binding region of non-human origin and a  
 CC portion of a human immunoglobulin. The humanized immunoglobulins are  
 CC useful for treating autoimmune diseases, infectious diseases,  
 CC inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 CC  
 XX  
 SQ Sequence 135 AA;  
 XX  
 QY 1 MGNWCIIFLVTATGVSQVQLVQSGAEVKKPSSSVKSCASGYPTDVAIQMWRQAP 60  
 Db 1 mgwncilflvtatgvsqqlvqsgaevkkpsssvkscasgyftdyaiqwrqap 60  
 QY 61 GGGLEWIGVINIYDNTNYNQKFKGKATMVDKSTAYMELSLRSEDVAVYCARAAW 120  
 Db 61 ggglewigvinilydntnynqgkfkgaatmvdksctaymelslrsedtavycaraaw 120  
 QY 121 YMDYWGOGTLVTSS 135  
 XX  
 RESULT 2  
 B07963  
 ID B07963 standard: Protein: 135 AA;  
 XX  
 AC B07963;  
 XX  
 DT 14-NOV-2000 (first entry)  
 XX  
 DE Amino acid sequence of heavy chain variable region of 3S1 antibody.  
 XX  
 XX Antibody 3D1: B7 molecule; B7: humanised immunoglobulin;  
 KW autoimmune disease; infectious disease; inflammatory disorder;  
 KW systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;  
 KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;

Db 121 ymdywgqgtsvsvs 135

## RESULT 3

W90935 standard; Protein; 470 AA.

W90935;

08-AUG-2000 (first entry)

Humanised anti-Fas designed heavy chain Heu 3 protein.

Fas: antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas; hepatotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Synthetic.

EP90663-A2.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

30-SEP-1998; 98JP-0276881.

30-SEP-1998; 98JP-0276882.

(SANY ) SANKYO CO LTD.

Setizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

WPI: 2000-258930/23.

N-PSDB: A11646.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 2; Page 180-182; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thymimetic, antirheumatic, hepatotropic, antinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic

CC the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 3

CC which is described in the method of the invention.

CC SQ Sequence 470 AA;

Query Match 81.3%; Score 585.5; DB 21; Length 470;

Best Local Similarity 81.4%; Pred. No. 3.5e-43;

Matches 114; Conservative 6; Mismatches 15; Indels 5; Gaps 1;

QY 1 MGNMCIIFFLVTTATGVSHQSOVLVOSGAEVKKRPGSSVKKVSCASGTTFTDYAIQWVROAP 60  
 DB 1 mgwscillifvatagvhsqvgqlvsgaeavkkpgasvkvscasytftfismqvwvrgap 60  
 QY 61 GGGLEWIGVINYDNTNYNOKFKATVTYDKSTSTAVMELSLRSEDFTAVYYCARAA- 119  
 DB 61 ggglewmgelgdsdyslynyqkfkqkatltvdststetaymelslrscdtavyycaarnrd 120  
 QY 120 ----WYMDYWGCGTLVTVSS 135  
 DB 121 ysnmyfdwvqgqlvtvss 140

## RESULT 4

W90933 standard; Protein; 470 AA.

W90933;

08-AUG-2000 (first entry)

Humanised anti-Fas designed heavy chain Heu 1 protein.

Fas: antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas; hepatotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Synthetic.

EP90663-A2.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

30-SEP-1998; 98JP-0276881.

30-SEP-1998; 98JP-0276882.

(SANY ) SANKYO CO LTD.

Setizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

WPI: 2000-258930/23.

N-PSDB: A11644.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 2; Page 169-170; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thymomimetic,  
 CC antineumatic, nephrotropic, antinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiac and hepatropic activity. (1) Induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (1) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (1) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (1) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 1  
 CC which is described in the method of the invention.

CC XX Sequence 470 AA:

Query Match 80.9%; Score 582.5; DB 21; Length 470;

Best Local Similarity 80.7%; Pred. No. 6.3e-43; Indels 5; Gaps 1;

Matches 113; Conservative 7; Mismatches 15;

QY 1 MGWNCIIFLVTATGVSQVQLVQSGAEVKKPKSSVKVSCAKSGYFTDTAIGWVQAP 60  
 CC [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]  
 CC 1 mgsccillflvatatgyhsqqlvgsaevkkpgasvksckasgyfltsymmqwvqgap 60

QY 61 GQGLEWIGVINIYDNTNRYNOKFKGKATMTVDKSTAYWELSLREDPAAVYVCARAA- 119  
 CC [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]  
 CC 61 gqglewmgelidpsdysynqkfkqgkattlvdststajmelslrsedtavyyccarnrd 120

QY 120 ----WYMDYWGCGTLVTVSS 135  
 CC [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]  
 CC Db 121 ysnmwyfdvvgqglvltvss 140

RESULT 5

W90934 ID W90934 standard; Protein: 470 AA.

AC W90934:

DT 08-AUG-2000 (first entry)

DE Humanised anti-Fas designed heavy chain Heu 2 protein.

XX XX Fas: antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiac;  
 KW dermatological; immunosuppressive; thymomimetic; antineumatic; anti-Fas;  
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX XX Synthetic.

OS EP990663-A2;

PN 05-APR-2000.

XX XX 29-SEP-1999; 99EP-0307711.  
 PF 30-SEP-1998; 98JP-0276681.  
 PR 30-SEP-1998; 98JP-0276682.  
 XX XX (SANY ) SANKYO CO LTD.

PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

DR WPI: 2000-258930/23;

DR N-PSDB: A11645.

XX XX New humanized anti-Fas antibody, useful for treating or preventing e.g.

PT inflammatory or autoimmune disease, induces apoptosis selectively in

PT cells with abnormal Fas-Fas ligand systems

PS Claim 2 : Page 174-176; 263pp; English.

XX XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thymomimetic,  
 CC antineumatic, nephrotropic, antinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiac and hepatropic activity. (1) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (1) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (1) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (1) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 2  
 CC which is described in the method of the invention.

XX XX Sequence 470 AA:

Query Match 80.8%; Score 581.5; DB 21; Length 470;

Best Local Similarity 80.7%; Pred. No. 7.7e-43; Indels 5; Gaps 1;

Matches 113; Conservative 7; Mismatches 15;

QY 1 MGWNCIIFLVTATGVSQVQLVQSGAEVKKPKSSVKVSCAKSGYFTDTAIGWVQAP 60  
 CC [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]  
 CC 1 mgsccillflvatatgyhsqqlvgsaevkkpgasvksckasgyfltsymmqwvqgap 60

QY 61 GQGLEWIGVINIYDNTNRYNOKFKGKATMTVDKSTAYWELSLREDPAAVYVCARAA- 119  
 CC [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]  
 CC 61 gqglewmgelidpsdysynqkfkqgkattlvdststajmelslrsedtavyyccarnrd 120

QY 120 ----WYMDYWGCGTLVTVSS 135  
 CC [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]  
 CC Db 121 ysnmwyfdvvgqglvltvss 140

RESULT 6

W83037 ID W83037 standard; Protein: 470 AA.

AC W83037;

XX XX



DT		1 <sup>st</sup> -MAR-1999	(first entry)
DE	XX	Anti-Fas humanised antibody HFE7A heavy chain.	
KW	XX	HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;	
KM	XX	apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;	
KW	XX	systemic lupus erythematosus; graft versus host disease;	
KW	XX	Sjogren syndrome; pernicious anaemia; Addison's disease;	
KW	XX	scleroderma; Goodpasture syndrome; Crohn's disease; sterility;	
KW	XX	rheumatoid arthritis; autoimmune haemolytic anaemia;	
KW	XX	amyotonia gravis; multiple sclerosis; Basedow's disease;	
KW	XX	thrombopenia purpura; insulin dependent diabetes; allergy;	
KW	XX	atopy; arteriosclerosis; myocarditis; cardiomyopathy;	
KW	XX	glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;	
KW	XX	transplant rejection; therapy.	
OS	XX	Homo sapiens.	
OS	XX	Synthetic.	
FH	FT	Key	Location/Qualifiers
FT	FT	Peptide	1..19
FT	FT	/label= Sig.peptide	
FT	FT	Protein	20..470
FT	FT	/label= Mat.protein	
FT	FT	Region	20..140
FT	FT	/label= Variable	
FT	FT	Region	141..464
FT	FT	/label= Constant	
FT	FT	Region	50..54
FT	FT	/label= CDR_H1	
FT	FT	/note= "claim 9"	
FT	FT	Region	69..84
FT	FT	/label= CDR_H2	
FT	FT	/note= "claim 9"	
FT	FT	Region	118..129
FT	FT	/label= CDR_H3	
FT	FT	/note= "claim 9"	
PN	PN	AU9859701-A.	
PD	PD	08-OCT-1998.	
XX	XX		
XX	PP	30-MAR-1998;	98AU-0059701.
XX	XX		
PR	PR	08-OCT-1997;	97JP-0276064.
PR	PR	01-APR-1997;	97JP-0082953.
PR	PR	25-JUN-1997;	97JP-0165088.
XX	XX		
PA	PA	(SANY ) SANKYO CO LTD.	
PI	PI	AKIO S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;	
PI	PI	Masahiko O, Nobutaka S, Shin Y, Tokuo T;	
DR	DR	WPI: 1998-543440/47.	
XX	XX	N-PDSB; V70080.	
PT	PT	New antibodies and proteins bind conserved epitope of Fas antigen -	
PT	PT	used to evaluate drugs in animal models and to treat Fas-associated	
PT	PT	diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis	
PT	PT	myocarditis, hepatitis and AIDS	
XX	XX		
XX	XX	Claim 22; Page 225-227; 292pp; English.	
CC	CC	This is the amino acid sequence of the HV type humanised heavy	
CC	CC	chain of murine anti-human Fas monoclonal antibody HFE7A. It	
CC	CC	includes humanising R44G and A76T amino acid substitutions that are	
CC	CC	conserved in the human IgG heavy chain. Host Escherichia coli	
CC	CC	pGPBDV3 SANK 70298 harbors plasmid pGPBDV3 carrying a fusion	
CC	CC	fragment of the humanised HV type HFE7A heavy chain and DNA	
CC	CC	fragment of human IgG1 constant region (see V70080), and is deposited	
CC	CC	as FERM BP-6273 (claimed). The invention provides methods for	
CC	CC	producing humanised antibodies by culturing host cells. Humanised	
CC	CC	versions of HFE7A (see WB3031-37), like native HFE7A, are capable	

CC	The invention relates to compositions for the prevention or treatment
CC	or diseases caused by an abnormality in the Fas/Fas ligand system
CC	containing an anti-Fas antibody as the active component. The anti-Fas
CC	antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC	or a humanised version of HFE7A containing identical CDRs
CC	(complementarily determining regions) to antibody HFE7A. Via its
CC	interaction with Fas, the antibody of the invention acts as a modulator
CC	of apoptosis. The compositions of the invention may therefore be used in
CC	the treatment or prevention of conditions such as autoimmune diseases..
CC	allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC	glomerulonephritis, aplastic anaemia (parmyelophthisis), hepatitis, AIDS
CC	and organ graft rejection. Sequences B14775-B14776 and B14779
CC	represent the heavy chains (or fragments thereof) of various humanised
CC	HFE7A-derived anti-Fas antibodies.
CC	
SQ	Sequence 470 AA:
	Query Match 80.5%; Score 579.5; DB 21; Length 470;
	Best Local Similarity 80.0%; Pred. No. 1,1e-42;
	Matches 112; Conservative 8; Mismatches 15; Indels 5; Gaps 1
Dy	1 MGACIIIFELVTTATGCHSOVLVOSAEYKRGSSVKYSCASGYTFDVAIQWRAP 60
Dy	1 MGWSCIILFIVATgshsqvqlvgsgaeekkpqgsavksvcasgytlfysymwqvkkap 60
Dy	61 GGCEMIIGVINIYYNDNTNNOEKFKATMYVDKSTTAAMELSSLSEPTAYYYCARAA- 119
Dy	61 ggglewmgeidpspsynngkfkykcaltlvdstetaymeislrsedttavyccarrd 120
Oy	120 ----WMDYWGCGTLVTSS 135
Dy	121 ysnmwyfdvwgeglvtlvs 140
RESULT	8
W90929	W90929 standard; Protein; 470 AA.
XX	W90929;
DT	08-AUG-2000 (first entry)
DE	Humanised HFE7A designed heavy chain protein #2.
Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;	
anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiac;	
dermatological; immunosuppressive; thyromimetic; antithematic; anti-Fas	
hepatotropic; antifertility; neuroprotective; antiartherosclerotic;	
hepatotrophic; humanized; apoptosis; systemic lupus erythematosus;	
Hashimoto disease; rheumatoid arthritis; graft versus host disease;	
Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;	
Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;	
multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;	
insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;	
cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.	
Synthetic.	
EP990663-A2.	
05-APR-2000.	
29-SEP-1999; 99EP-0307711.	
30-SEP-1998; 98JP-0276681.	
30-SEP-1998; 98JP-0276682.	
(SANKYO CO LTD.	
Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;	
WPI; 2000-258930/23.	

N-PSDB:A11622.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Example reference 22; Page 150-152; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thymometric, antirheumatic, nephroprotective, antifertility, neuroprotective, anticardiosclerotic, cardiact and hepatotropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombocytopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (II) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HEF7A designed heavy chain which is used in the method described in the invention.

Sequence 470 AA:

Query Match 80.5%; Score 579.5; DB 21; Length 470;  
Best Local Similarity 80.0%; Pred. No. 1.le-42;  
Matches 112; Conservative 8; Mismatches 15; Indels 5; Gaps 1

1 MGNWCIIFPLVTTATGVMHSQVDLVNOSGAETKPKGSYKVCASACGYTFPDYAIOAWRQAP 60  
|||||  
1 mgswwcillflvalatagvsqglvsgaeavkkpgasvkvscasygtlftsygmwkwkqap 60

61 GGGLFMIGIVINYYNTNNOKFKAGTAYTVKSTAVAMELSLSEPTAAVYCCARAA- 119  
|||||  
61 ggglemmeidspsdytlnynqkfkgkatltvtstctajameislrsedtavayccarnd 120

120 ---WYMDWGCGTLVTYSS 135  
|||  
121 ysnwyfdwggeqltvtsas 140

R55556 standard; Protein: 140 AA.  
R55556:  
R55556:  
16-NOV-1994 (first entry)  
DRGC-200 Humanized antibody heavy chain variable region.  
DREG-200; I-selectin; LECAM-1; Mel-14; TAM-1;  
humanized antibody; immunoglobulin; Ig; IGg1; IGg4;  
complementarity determining region; CDR; monoclonal antibody; Mab;  
framework; light chain; heavy chain; variable domain;  
monoclonal antibody; acceptor antibody Eu; Transgenic animal.  
Mus sp.; Homo sapiens.

```
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label- Sig-peptide
FT Region 50..54
FT /label- CDR1
FT Region 69..85
FT /label- CDR2
FT Region 118..129
FT /label- CDR3
XX
XX W09412215-A.
XX
XX 09-JUN-1994.
XX
XX 30-NOV-1993; 93WO-US11612.
XX
XX 01-DEC-1992; 92US-0983946.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Co MS:
XX
XX WPI: 1994-199974/24.
XX
XX N-PSDB: Q66702.
XX
XX New humanised antibody specific for L-selectin - with murine CDR
XX and human framework regions, inhibits binding of neutrophils to
XX endothelial cells and useful for treating or preventing
XX inflammation
XX
XX Disclosure: Fig. 3B; 60pp; English.
XX
XX An L-selectin-specific IgG1 or IgG4 humanized antibody has CDRs
XX corresponding to those of mouse Mab DREG-200 and heavy and light
XX chain variable region frameworks of the human acceptor antibody Eu.
XX Nucleotide and aa sequences are provided for the DREG-200 light
XX (Q66699, R55553) and heavy (Q66700, R55554) chain variable regions
XX and the humanized DREG-200 light (Q66701, R55555) and heavy (Q66702,
XX R55556) chain variable regions. The humanized antibodies can be
XX produced economically in large quantities by expression in mammalian
XX cell culture or in transgenic animals.
XX
XX Sequence 140 AA:
XX
XX Query Match 79.7%; Score 573.5; DB 15; Length 140;
XX Best Local Similarity 78.6%; Pred. No. 1.1e-42;
XX Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;
```

```
KM Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KM anti-allergic; anti-arthritic; antiviral; immunomodulatory; candid;
KM dermatological; immunosuppressive; thymic; antirheumatic; anti-Fas;
KM neoplastic; antileukemic; neuroprotective; antileukemic; anti-Fas;
KM hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KM Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KM Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
KM Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KM multiple sclerosis; Basedow's disease; thrombocytopenia purpura; allergy;
KM insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KM cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
XX Synthetic.
XX
XX EP930663-A2.
XX
XX 05-APR-2000.
XX
XX 29-SEP-1999; 99EP-0307711.
XX
XX 30-SEP-1998; 98JP-0276881.
XX
XX 30-SEP-1998; 98JP-0276882.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Serizawa N, Haryama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI: 2000-258930/23.
XX
XX N-PSDB: A11655.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems
XX
XX Claim 2; Page 188-189; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
XX ligand system, by binding to Fas on the cell surface, and prevents
XX apoptosis in cells with a normal system, by inhibiting binding between
XX Fas and its ligand. The products of the invention have anti-inflammatory,
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
XX immunomodulatory, dermatological, immunosuppressive, thymic,
XX antirheumatic, hepatotropic, antileukemic, neuroprotective,
XX antiarteriosclerotic, candid and hepatotropic activity. (I) induce
XX apoptosis by binding to cell surface Fas or inhibit it by competitive
XX inhibition of ligand binding. (I) are used to treat and/or prevent
XX diseases associated with the Fas/Fas ligand system, especially systemic
XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
XX versus host disease, Sjogren's syndrome, peritonitis or hypoplastic
XX anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
XX disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
XX multiple sclerosis, Basedow's disease, thrombocytopenia purpura, insulin
XX dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
XX cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
XX (B, C or D) or alcoholic), and transplant rejection. (I) selectively
XX inhibit apoptosis in normal cells but selectively induce it in abnormal
XX cells. They bind to both human and murine Fas, so can be evaluated in
XX murine disease models. (I) act on the active site of Fas, i.e. they mimic
XX the native ligand, do not induce liver disease, and have reduced risk of
XX inducing a human anti-murine antibody response. This sequence represents
XX a humanised anti-Fas antibody HFE7A heavy chain construct HHH type
XX which is described in the method of the invention.
XX
XX Sequence 470 AA:
XX
XX Query Match 78.8%; Score 567.5; DB 21; Length 470;
XX Best Local Similarity 78.6%; Pred. No. 1.3e-41;
XX Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;
```

[illegible]

xx ps  cc CC	  Example 3; Page 207; 292pp; English.  This is the amino acid sequence of the VD type humanised heavy chain variable region of murine anti-human Fas monoclonal antibody HFE7A. It was utilised in a claimed humanised HFE7A heavy chain (see V70079). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see W830331-37) are capable of inducing apoptosis in abnormal cells expressing fas, and/or inhibiting fas-induced apoptosis in normal cells. Humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
xx SQ  Query Match Best Local Similarity Matches 110;	 Sequence 145 AA;  78.7%; Score 566.5; DB 19; Length 145; 78.6%; Pred. No. 4.5e-42; Conservative 8; Mismatches 17; Indels 5; Gaps 1;
OY	1 MGNMCIIFELVTATGCHSVQVQLVDSGEVKKPGSSAVVSCKASGYTFTDYAIOWRQAP 60
Dd	1 mgschllflvalatagvhsqqlvgsgaevkkgpasvsvskasygtlftsymgmwvxgdp 60
OY	61 GGCGEIMICVINIYYNTNWNOKFKAMPTMDKSTSYMEISSLRSDTFVVYCARRAA- 119
Dd	61 ggrlewmgeipdsdytnynqkfkygakltlvdstastaymelslrsestdavyycarrnd 120
OY	120 ---WYMDYWGGCTLVTVSS 135
Dd	121 ysnmyfdgwgegltvtvs 140
RESULT 12	
B14775	B14775 standard; peptide; 145 AA.
ID	
AC	B14775;
XX	
DT	24-NOV-2000 (first entry)
DE	Fragment of humanised anti-Fas antibody heavy chain, SEQ ID NO:75.
XX	
KW	Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BF-5828;
KW	murine; humanised antibody; complementarity determining region; CDR;
KW	human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW	autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW	cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
KW	hepatitis; AIDS; graft rejection; heavy chain.
OS	Chimeric - Mus musculus.
OS	Chimeric - Homo sapiens.
XX	
PM	JP2000169393-A.
PD	20-JUN-2000.
Pf	30-SEP-1999; 99JP-0278301.
PR	30-SEP-1998; 98JP-0276883.
PA	(SANY ) SANKYO CO LTD.
WI	WPI: 2000-485645/43.

DR N-PSDB: A72146.

XX Preventive or treating agent for the diseases caused by an abnormality  
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 PT anti-Fas antibody

PS Example 15; Page 88; 139pp; Japanese.

XX The invention relates to compositions for the prevention or treatment  
 CC or diseases caused by an abnormality in the Fas/Fas ligand system  
 CC containing an anti-Fas antibody as the active component. The anti-Fas  
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 CC or a humanised version of HFE7A containing identical CDRs  
 CC (complementarity determining regions) to antibody HFE7A. Via its  
 CC interaction with Fas, the antibody of the invention acts as a modulator  
 CC of apoptosis. The compositions of the invention may therefore be used in  
 CC the treatment or prevention of conditions such as autoimmune diseases,  
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 CC and organ graft rejection. Sequences B1475-B1476 and B14779  
 CC represent the heavy chains (or fragments thereof) of various humanised  
 CC HFE7A-derived anti-Fas antibodies.

XX Sequence 145 AA;

SO Query Match 78.7%; Score 566.5; DB 21; Length 145;  
 Best Local Similarity 78.6%; Pred. No. 4.5e-42;  
 Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

OY 1 MGNMCIIFLVTTATGCHSVQVQVSGAEVKKRPGSSVKVSKASGTYTFDYAIQWVRQAP 60

DB 1 MGWSCHLLIFVATAGVHSQVGLVSGAEVKKPGASVKSCASGYTLFTSYMMQVWKQAP 60

OY 61 GGGLEWIGVINIYDNTNNOKFKKATMTVDKSTSTAYMELSLSEDPAYVYCARAA- 119

DB 61 GGRLEWIGVIGDPSDYTNNGKFKKATLTVDLSASTAYMELSLRSDTAYVYCAARNR 120

OY 120 ---WTMDYWGQGTIVTVSS 135

DB 121 YSNWYFDVWGEGTLTVSS 140

OY 121 YSNWYFDVWGEGTLTVSS 140

DB 121 YSNWYFDVWGEGTLTVSS 140

OY 121 YSNWYFDVWGEGTLTVSS 140

DB 121 YSNWYFDVWGEGTLTVSS 140

OY 121 YSNWYFDVWGEGTLTVSS 140

DB 121 YSNWYFDVWGEGTLTVSS 140

OY 121 YSNWYFDVWGEGTLTVSS 140

DB 121 YSNWYFDVWGEGTLTVSS 140

OY 121 YSNWYFDVWGEGTLTVSS 140

DB 121 YSNWYFDVWGEGTLTVSS 140

OY 121 YSNWYFDVWGEGTLTVSS 140

DB 121 YSNWYFDVWGEGTLTVSS 140

OY 121 YSNWYFDVWGEGTLTVSS 140

DB 121 YSNWYFDVWGEGTLTVSS 140

OY 121 YSNWYFDVWGEGTLTVSS 140

PR 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.

XX (SANY ) SANKYO CO LTD.

PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI: 2000-258930/23.

DR N-PSDB: A11584.

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems

PS Example reference 15; Page 126-127; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antihumetic, nephroprotective, antineoplastic, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody HFE7A heavy chain which is used in  
 CC the method described in the invention.

SO Sequence 145 AA;

SO Query Match 78.7%; Score 566.5; DB 21; Length 145;  
 Best Local Similarity 78.6%; Pred. No. 4.5e-42;  
 Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

OY 1 MGNMCIIFLVTTATGCHSVQVQVSGAEVKKRPGSSVKVSKASGTYTFDYAIQWVRQAP 60

DB 1 MGWSCHLLIFVATAGVHSQVGLVSGAEVKKPGASVKSCASGYTLFTSYMMQVWKQAP 60

OY 61 GGGLEWIGVINIYDNTNNOKFKKATMTVDKSTSTAYMELSLSEDPAYVYCARAA- 119

DB 61 GGRLEWIGVIGDPSDYTNNGKFKKATLTVDLSASTAYMELSLRSDTAYVYCAARNR 120

OY 120 ---WTMDYWGQGTIVTVSS 135

DB 121 YSNWYFDVWGEGTLTVSS 140

OY 121 YSNWYFDVWGEGTLTVSS 140

DB 121 YSNWYFDVWGEGTLTVSS 140

OY 121 YSNWYFDVWGEGTLTVSS 140

DB 121 YSNWYFDVWGEGTLTVSS 140

OY 121 YSNWYFDVWGEGTLTVSS 140

DB 121 YSNWYFDVWGEGTLTVSS 140

XX	HEF7A: monoclonal antibody; mouse; Fas; humanised antibody;
KW	apoptosis; HEF7A; autoimmune disease; Hashimoto's disease;
KW	systemic lupus erythematosus; graft versus host disease;
KW	Sjogren syndrome; perniciouss anaemia; Addison's disease;
KW	scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW	rheumatoid arthritis; autoimmune haemolytic anaemia;
KW	myasthenia gravis; multiple sclerosis; Basedow's disease;
KW	thrombopenia purpura; insulin-dependent diabetes; allergy;
KW	atrophy; arteriosclerosis; myocarditis; cardiomyopathy;
KW	glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW	transplant rejection; therapy.
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	Peptide
FT	/label= Sig.peptide
FT	20..470
FT	/label= Mat.protein
FT	20..140
FT	/label= Variable
FT	141..464
FT	/label= Constant
FT	50..54
FT	/label= CDR_H1
FT	/note= "claim 9"
FT	69..84
FT	/label= CDR_H2
FT	/note= "claim 9"
FT	118..129
FT	/label= CDR_H3
FT	/note= "claim 9"
XX	
PN	AU9859701-A.
PD	
XX	08-OCT-1998.
PD	
XX	30-MAR-1998; 98AU-0059701.
PF	
PR	08-OCT-1997; 97JP-0276064.
PR	01-APR-1997; 97JP-0082953.
PR	25-JUN-1997; 97JP-0165088.
XX	
PA	(SANY ) SANKYO CO LTD.
PI	
PI	Atto S., Hideyuki H., Hiroko Y., Jun O., Kimihisa I;
PI	Masahiko O., Nobufusa S., Shin Y., Tohru T;
DR	
XX	WPI; 1998-543440/47.
DR	N-PSDB; V70079.
PT	
PT	New antibodies and proteins bind conserved epitope of Fas antigen -
PT	used to evaluate drugs in animal models and to treat fas-associated
PT	diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
PT	myocarditis, hepatitis and AIDS
XX	
PS	Claim 22; Page 212-213; 292pp; English.
XX	
CC	This is the amino acid sequence of the VD type humanised heavy
CC	chain of murine anti-human Fas monoclonal antibody HEF7A. E. coli
CC	expression vector pGSL7A62 carrying a fusion
CC	fragment of the humanised VD type HEF7A heavy chain and DNA
CC	encoding human IgG1 constant region (see V70079) and is deposited
CC	as FERM BP-6074 (claimed). The invention provides methods for
CC	producing humanised antibodies by culturing host cells. Humanised
CC	versions of HEF7A (see W83031-37), like native HEF7A, are capable
CC	of inducing apoptosis in abnormal cells expressing Fas, and of
CC	inhibiting Fas-induced apoptosis in normal cells. The humanised
CC	antibodies are used to evaluate, in animal models, treatments of
CC	diseases that involve Fas/Fas ligand interactions, and also to
CC	treat such diseases, including autoimmune disease (e.g. systemic

[illegible]

CC (complementarily determining regions) to antibody HFE7A. Via its  
 CC interaction with Fas, the antibody of the invention acts as a modulator  
 CC of apoptosis. The compositions of the invention may therefore be used in  
 CC the treatment or prevention of conditions such as autoimmune diseases,  
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 CC and organ graft rejection. Sequences B1475-B1476 and B14779  
 CC represent the heavy chains (or fragments thereof) of various humanised  
 CC HFE7A-derived anti-Fas antibodies.  
 XX

SQ Sequence 470 AA:

Query Match 78.7%; Score 566.5; DB 21; Length 470;  
 Best Local Similarity 78.6%; Pred. No. 1.5e-41;  
 Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

OY 1 MGNMCIIFFLVYTATGVHSQVQLVQSGAEVKKRQSSVKVSKCKASGYTFDVAIQWVQAP 60  
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1 mgwscililflvalatavhsqvgllvgsgeevkkgasvkvskasgytlftsymgwkqap 60  
 OY 61 GQGLEWIGVINIYDNTYNQKFKGKATMTVDKSTSTAYMEISSLRSEPTAVYCCARAA- 119  
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 61 gqrlwemgeidpsdsytynqgfkgtkaltlvdsastaymeislrseclavycarnrd 120  
 OY 120 ---WYMDYWGOGTLTVSS 135  
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 Db 121 ysnwvfdwvgeglvtvss 140

Search completed: April 25, 2001, 09:37:50  
 Job time: 68 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2001, 09:36:42 ; Search time 20.89 Seconds  
(without alignments)  
124.149 Million cell updates/sec

Title: US-09-249-011-6  
Perfect score: 720  
Sequence: 1 MGNMCIFFLVTTATGVHSQ.....APAAWYMDYGGGTLTVSS 135

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PCITUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573.5	79.7	140	US-08-579-378A-12	Sequence 12, Appl
2	573.5	79.7	140	PCIT-US93-11612-12	Sequence 12, Appl
3	545	75.7	135	US-07-634-278-19	Sequence 19, Appl
4	545	75.7	135	US-08-477-728-19	Sequence 19, Appl
5	545	75.7	135	US-08-474-040-19	Sequence 19, Appl
6	545	75.7	135	US-08-487-200-19	Sequence 19, Appl
7	545	75.7	135	US-08-303-569B-31	Sequence 31, Appl
8	545	75.7	135	US-08-484-537-19	Sequence 19, Appl
9	531.5	73.8	163	PCIT-US91-02942-5	Sequence 5, Appl
10	530.5	73.7	140	US-08-836-561-63	Sequence 63, Appl
11	530	73.6	467	US-07-916-098A-45	Sequence 45, Appl
12	529.5	73.5	136	PCIT-US93-11611-11	Sequence 11, Appl
13	529.5	73.5	136	US-08-513-968-44	Sequence 44, Appl
14	529	73.5	139	US-08-656-586-8	Sequence 8, Appl
15	527	73.2	135	US-08-137-117D-102	Sequence 102, Appl
16	527	73.2	135	US-08-436-717-102	Sequence 102, Appl
17	526	73.1	133	US-08-718-323A-8	Sequence 8, Appl
18	525	72.9	139	US-08-253-877C-19	Sequence 19, Appl
19	525	72.9	139	US-08-452-164A-19	Sequence 19, Appl
20	525	72.9	139	US-08-603-024-18	Sequence 18, Appl
21	521	72.4	135	US-08-137-117D-100	Sequence 100, Appl
22	521	72.4	135	US-08-436-717-100	Sequence 100, Appl
23	521	72.4	137	US-08-513-968-38	Sequence 38, Appl
24	518.5	72.0	140	US-08-836-561-74	Sequence 74, Appl
25	515.5	71.6	140	US-08-836-561-78	Sequence 78, Appl
26	515	71.5	135	US-08-137-117D-112	Sequence 112, Appl
27	515	71.5	135	US-08-436-717-112	Sequence 112, Appl

28	508.5	70.6	143	1	US-08-236-520-7	Sequence 7, Appl
29	508.5	70.6	143	5	PCIT-US95-05262-7	Sequence 7, Appl
30	507.5	70.5	140	3	US-08-836-561-83	Sequence 83, Appl
31	503.5	69.9	140	1	US-07-946-421-28	Sequence 28, Appl
32	501.5	69.7	123	1	US-08-482-882-53	Sequence 53, Appl
33	501.5	69.7	123	2	US-08-483-389-53	Sequence 53, Appl
34	501.5	69.7	123	2	US-08-487-113D-53	Sequence 53, Appl
35	501.5	69.7	123	2	US-08-473-503-53	Sequence 53, Appl
36	501.5	69.7	123	2	US-08-483-932-53	Sequence 53, Appl
37	501.5	69.7	123	3	US-08-720-420A-53	Sequence 53, Appl
38	501.5	69.7	123	3	US-08-714-017-53	Sequence 53, Appl
39	501.5	69.7	123	3	US-08-475-680-53	Sequence 53, Appl
40	500.5	69.5	142	2	US-08-476-176B-14	Sequence 14, Appl
41	500.5	69.5	142	3	US-08-127-721A-14	Sequence 14, Appl
42	500.5	69.5	142	3	US-08-485-246A-14	Sequence 14, Appl
43	499	69.3	128	4	US-09-199-148-12	Sequence 12, Appl
44	498	69.2	116	1	US-07-634-278-57	Sequence 57, Appl
45	498	69.2	116	1	US-07-634-278-73	Sequence 73, Appl

#### ALIGNMENTS

RESULT 1  
US-08-579-378A-12  
Sequence 12, Application US/08579378A  
Patent No. 6210671  
GENERAL INFORMATION:  
APPLICANT: CO, Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
TITLE OF INVENTION: L-Selectin  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/579,378A  
FILING DATE: 27-DEC-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160,074  
FILING DATE: 30-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,946  
FILING DATE: 01-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95112895.8  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95114696.8  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebescheit, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 11823-002220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-579-378A-12

Query Match	79.78;	Score 573.5;	DB 4;	Length 140;
Best Local Similarity	78.68;	Pred. No. 2.9e-50;		
Matches 110; Conservative	8;	Mismatches 17;	Indels 5;	Gaps 1;

[illegible]

```

RESULT      2
PCT-US93-11612-12
; Sequence 12, Application PC/TUS9311612
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11612
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11623-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11612-12

```

Query Match	79.7%	Score 573.5	DB 5	Length 140
Best Local Similarity	78.6%	Pred. No. 2.9e-50		
Matches 110: Conservative	8	Mismatches 17	Indels 5	Gaps 1
QY	1	MGMNCIIFFELTTATGVSQVQLVDSGAEYVKRPGSSVSVSCASCATYETFDYAIQAWROAP	60	
Db	1	MGMSCIIELVATATGVSQVQLVDSGAEYVKRPGSSVSVSCASCATYETFTSYVMHMYRQAP	60	
QY	61	GGGLEWIGVNIYYDNTNINOKFKGATMYTDKSTSTAMELSSIRSEDTAVYTCARAAAP	120	

D<sub>b</sub>    61 GQGLEMIGIYIPYPNDGTRKYNKEFGRAVITTSDESTNTAYMELSLRSEDPAVIYCAREEY 120  
Q<sub>y</sub>    121 -----YMDYMGQGTLYTYSS 135  
               | + ||||| |||||  
D<sub>b</sub>    121 GNYYRYFDVMQGQGTLYTYSS 140

```

RESULT 3
US-07-634-278-19
: Sequence 19, Application US/07634278
: Patent No. 5530101
: GENERAL INFORMATION:
: APPLICANT: QUEEN, Cary L.
: APPLICANT: CO, Man Sung
: APPLICANT: SCHNEIDER, William P.
: APPLICANT: LANDOLFI, Nicholas F.
: APPLICANT: COELINGH, Kathleen L.
: APPLICANT: SELICK, Harold E.
: TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourile and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/634,278
: FILING DATE: 19-DEC-1990
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/590,274
: FILING DATE: 28-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/310,252
: FILING DATE: 13-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/290,975
: FILING DATE: 28-DEC-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-002600
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 135 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-634-278-19

```

Query Match	75.78;	Score 545;	DB 1;	Length 135;
Best Local Similarity	77.88;	Pred. NO. 2e-47;		
Matches 105; Conservative	7;	Mismatches 23;	Indels 0;	Gaps 0

[illegible]

QY	121	YMDYWGQGLVTVSS	135
Db	121	VFDYWGQGLVTVSS	135

```

RESULT 4
US-08-477-728-19
Sequence 19, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCE ADDRESSES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-728-19

```

```

Query Match 75.7%: Score 545; DB 1; Length 135;
Best Local Similarity 77.8%: Pred. No. 2e-47;
Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0

QY 1 MGNACIIFELVTATGCHSQVOLVOSGAEEVKKRGSSVKKVSCASGCTFTDVAIQWVRQAP 60
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 MGSWMIFFELLSAGTAGVHSQVOLVOSGAEEVKKRGSSVKKVSCASGCTFTFSYRMHWROAP 60
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 61 GGGEMIEGIVINLYYDNTNYNOKFKGAKMTYVTKSTSTAYMELSSLRSEPTAYYYCARAAM 120
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 GGGEMIEGIVINPSTCYTLEYNOKFKRAKITITADESNTNTAYMEISSLRSEPTAYYYCARGGC 120
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 121 YMDYWGCGTGLTVSS 135
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

Db          121.FDYWGQCTLVTVSS 135

RESULT      5
US-08-474-040-19
Sequence 19, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourlie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-040-19

```

```

Query Match      75.7%; Score 545; DB 1; Length 135;
Best Local Similarity 77.8%; Pred. No. 2e-47;
Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0.

QY      1  MGNMCIFFLVTTATGVSQVOLVOSGAEEVKRGGSSVKVSKASGYTFTDVAIQWVRAP 60
        ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       1  MGWSNIFLELTSGTAGVHSQVOLVOSGAEEVKRKGGSSVKKSCASGYTFPSYRNHWVRAP 60

QY      61  GGGEWMIVINYYNTNVNNOKFRKATPVTKRSTATAAMELSSLRSEPTAYYYCARAAW 120
        ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       61  GGGLEMTICVINPSTCYTEYNCKFRKATITADESINTATAMELSSLRSEPTAYYYCARGAG 120

QY      121 YMDWGCGTLTVVSS 135
        |||||||

```

Db 121 VEDYWGQGLTVSS 135

## RESULT 6

US-08-487-200-19

Sequence 19, Application US/08487200  
Patent No. 5693762

## GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: COELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,200

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-002610

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-487-200-19

Query Match

Best local similarity 75.7%; Score 545; DB 1; Length 135;

Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

## RESULT 7

US-08-303-569B-31

Sequence 31, Application US/08303569B  
Patent No. 5859205

## GENERAL INFORMATION:

APPLICANT: Adair, John R.

APPLICANT: Emage, John S.

APPLICANT: Humanised Antibodies

TITLE OF INVENTION: Humanised Antibodies

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESS: Woodcock Washburn Kurtz MacKiewicz &amp; NO. 5859205-115

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/303,569B

FILING DATE: 07-SEP-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Trujillo, Doreen Yalko

REGISTRATION NUMBER: 35,719

REFERENCE/DOCKET NUMBER: CARP-0032

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-303-569B-31

Query Match

Best local similarity 75.7%; Score 545; DB 2; Length 135;

Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135

Db 121 VEDYWGQGLTVSS 135

OY 121 VEDYWGQGLTVSS 135



ADDRESS: ALLEGRETTI & WINCOFF  
 STREET: 10 SOUTH WACKER DRIVE  
 CITY: CHICAGO  
 STATE: ILLINOIS  
 COUNTRY: U.S.A.  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.23  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11611  
FILING DATE: 30-NOV-1993  
CLASSIFICATION: 1  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,949  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.



Oy 1 MGNNCIIFLVTTATGVSQVOLVOSGAIEVKKPGSSVKVSKASGYTFTDYAIQWVROAP 60  
 Db 1 MGNMFWFLFLLSGTAGVHSQVOLVOSGAIEVKKPGASVSKVSKASGYTFTSYIHWVROAP 60  
 Oy 61 GGGLEMGIVINITYDNTNOKFKGKATMTVDKSTAYMELSLRSDEPTAVYICARAAW 120  
 Db 61 GGGLEMGIVINIPNSGYTHNOKLKDRAATLADKASASTAYMELSLRSDEPTAVYICARSAV 120  
 Oy 121 Y---MDYWGQGTFLVTSS 135  
 Db 121 YDYDGFAYWGQGTFLVTSS 139

RESULT 15  
 US-08-137-117D-102  
 : Sequence 102, Application US/08137117D  
 : Patent No. 5795965

GENERAL INFORMATION:  
 APPLICANT: TSUCHIYA, Masayuki  
 APPLICANT: SATO, Koh  
 APPLICANT: BENDIG, Mary  
 APPLICANT: JONES, Steven  
 APPLICANT: SALDANHA, Jose  
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
 TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
 NUMBER OF SEQUENCES: 158  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/137,117D  
 FILING DATE: 20-DEC-1993  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/JP92/00544  
 FILING DATE: 24-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 4-32084  
 FILING DATE: 19-FEB-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 3-95476  
 FILING DATE: 25-APR-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WEGNER, Harold C.  
 REGISTRATION NUMBER: 25,258  
 REFERENCE/DOCKET NUMBER: 53466/126/AOAK  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)672-5300  
 TELEFAX: (202)672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 102:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 135 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-137-117D-102

Query Match 73.2%; Score 527; DB 1; Length 135;  
 Best Local Similarity 75.6%; Pred. No. 1,2e-45;  
 Matches 102; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

Oy 1 MGNNCIIFLVTTATGVSQVOLVOSGAIEVKKPGSSVKVSKASGYTFTDYAIQWVROAP 60

Db 1 MGNMFWFLFLLSGTAGVHSQVOLVOSGAIEVKKPGASVSKVSKASGYTFTSYIHWVROAP 60  
 Oy 61 GGGLEMGIVINITYDNTNOKFKGKATMTVDKSTAYMELSLRSDEPTAVYICARAAW 120  
 Db 61 GGGLEMGIVIDPFGNGTSTNOKFKGKATMTVDKSTAYMELSLRSDEPTAVYICARAGN 120  
 Oy 121 YMDYWGQGTFLVTSS 135  
 Db 121 RFAYWGQGTFLVTSS 135

Search completed: April 25, 2001, 09:37:09  
 Job time: 27 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 20:35:05 ; Search time 1433.84 Seconds  
(without alignments)  
1700.705 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 396

Sequence: 1 atggtaccagcgcccggt.....ggaccacagtggaataaaa 396

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_in1:\*  
5: gb\_in2:\*  
6: gb\_in3:\*  
7: gb\_cm:\*  
8: gb\_ov:\*  
9: gb\_pat1:\*  
10: gb\_pat2:\*  
11: gb\_ph:\*  
12: gb\_pl1:\*  
13: gb\_pl2:\*  
14: gb\_pl3:\*  
15: gb\_pl4:\*  
16: em\_ba1:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
20: em\_htgo\_inv:\*  
21: em\_htgo\_rtd:\*  
22: em\_htg\_hum1:\*  
23: em\_htg\_hum2:\*  
24: em\_htg\_hum3:\*  
25: em\_htg\_hum4:\*  
26: em\_htg\_hum5:\*  
27: em\_htg\_hum6:\*  
28: em\_htg\_hum7:\*  
29: em\_htg\_hum8:\*  
30: em\_htg\_inv1:\*  
31: em\_htg\_inv2:\*  
32: em\_htg\_other:\*  
33: em\_htg\_rtd:\*  
34: em\_hum1:\*  
35: em\_hum2:\*  
36: em\_hum3:\*  
37: em\_hum4:\*  
38: em\_hum5:\*  
39: em\_hum6:\*  
40: em\_hum7:\*  
41: em\_in:\*  
42: em\_cm:\*  
43: em\_or:\*

44: em\_ov:\*  
45: em\_pat:\*  
46: em\_ph:\*  
47: em\_pl:\*  
48: em\_ro:\*  
49: em\_sts:\*  
50: em\_sy:\*  
51: em\_un:\*  
52: em\_vi:\*  
53: gb\_sts1:\*  
54: gb\_sts2:\*  
55: gb\_sts3:\*  
56: gb\_sy:\*  
57: gb\_un:\*  
58: gb\_vil:\*  
59: gb\_vil2:\*  
60: gb\_vil3:\*  
61: gb\_vil4:\*  
62: gb\_vil5:\*  
63: gb\_vil6:\*  
64: gb\_vil7:\*  
65: gb\_vil8:\*  
66: gb\_vil9:\*  
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69: gb\_vil12:\*  
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73: gb\_vil16:\*  
74: gb\_vil17:\*  
75: gb\_vil18:\*  
76: gb\_vil19:\*  
77: gb\_vil20:\*  
78: gb\_vil21:\*  
79: gb\_vil22:\*  
80: gb\_vil23:\*  
81: gb\_vil24:\*  
82: gb\_vil25:\*  
83: gb\_vil26:\*  
84: gb\_vil27:\*  
85: gb\_vil28:\*  
86: gb\_vil29:\*  
87: gb\_vil30:\*  
88: gb\_vil31:\*  
89: gb\_vil32:\*  
90: gb\_vil33:\*  
91: gb\_vil34:\*  
92: gb\_vil35:\*  
93: gb\_vil36:\*  
94: gb\_vil37:\*  
95: gb\_vil38:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340	85.9	462	94	M28833 Mus musculus
2	340	85.9	480	9	A13733 variable re
3	336.2	84.9	406	94	M062050 Mus musculus
4	333.6	84.2	419	94	MM097570 Mus musculus
5	332	83.8	940	9	A44968 Sequence 24
6	332	83.8	940	10	I64459
7	301.4	76.1	401	94	MM1211EV
8	298.2	75.3	402	94	M98042 Mouse Ig re
9	296	74.7	336	94	AF163745 Mus muscu
10	296	74.7	336	94	MD1GVAR
11	296	74.7	339	94	AB028876 Mus muscu

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12 295.2 74.5 408 95 S81289
13 295 74.5 336 94 MUSICKV130
14 292.8 73.9 336 94 MDIGKAV1
15 292.8 73.9 336 94 MDIGKAVU
16 288.6 72.9 339 9 A47611
17 288.6 72.9 339 9 A80111
18 286.4 72.3 336 94 MMJ222607
19 286.4 72.3 337 95 A62621
20 285.4 72.1 439 9 A62621
21 285.4 72.1 460 9 A62617
22 284.8 71.9 336 94 MMKACTV
23 284.8 71.9 336 94 MUSICKADV
24 284.8 71.9 339 94 MMU060464
25 284.8 71.9 336 94 MMU05673
26 284.2 71.8 336 94 MMU05674
27 284.2 71.8 336 94 MDIGKAVU
28 283.2 71.5 336 94 MMU15982
29 281.8 71.2 764 94 MMU15982
30 281.4 71.1 336 94 MMU05673
31 280.6 70.9 399 94 MUSFABA
32 279.8 70.7 411 94 MMIGCVJ5
33 279.8 70.7 1443 9 AR063210
34 279 70.5 427 9 A94042
35 279 70.5 427 9 AX011127
36 279 70.5 463 9 AX011127
37 279 70.5 8068 9 A94046
38 279 70.5 8068 9 AX011131
39 278.4 70.3 336 94 MUSICKADM
40 278 70.2 336 94 MMU05675
41 277.8 70.2 747 56 AC0131533
42 277.6 70.1 336 94 MDIGKAVB
43 277.2 70.0 881 94 MDIGKAVB
44 276.6 69.8 348 94 AF232221
45 275.8 69.6 870 9 AR063208
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## ALIGNMENTS

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881289 Igm kappa c
L16819 Mus musculus
Z22039 M.domesticu
Z22070 M.domesticu
A47611 Sequence 3
A80111 Sequence 3
AJ222607 mouse DNA
S74056 Iq VKI-1952
A62621 Sequence 40
A62617 Sequence 36
Z31353 M.musculus
M37022 Mouse Iq re
M37023 Mouse Iq re
U60464 Mus musculu
U55647 Mus musculu
U55674 Mus musculu
Z22060 M.domesticu
Y13982 Mus musculu
M95673 Mus musculu
M95674 M.musculus
X02181 M.musculus
AR063210 Sequence
A94042 Sequence 23
AX011127 Sequence
AR109948 Sequence
A94046 Sequence 27
AX011131 Sequence
M37024 Mouse Iq re
U55675 Mus musculu
AJ131533 Synthetic
Z22023 M.domesticu
L27438 Mouse Immun
AF232221 Mus muscu
AR063208 Sequence
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RESULT 1
LOCUS MUSICKPALI 462 bp mRNA ROD 18-NOV-1994
DEFINITION Mus musculus Iq chain (anti-Pseudomonas aeruginosa lipoprotein I
ACCESSION M28833
VERSION M28833.1 GI:576599
KEYWORDS V-segment; anti-lipoprotein antibody; immunoglobulin kappa-chain;
immunoglobulin light chain.
SOURCE Mus musculus (strain BALB/c, sub-species domesticus) hybridoma CDNA
to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 462)
AUTHORS Margel,M., Eckhardt,A., Ehret,M., von Specht,B.U., Duchene,M. and
Domdey,H.
TITLE Cloning and characterization of cDNAs coding for the heavy and
light chains of a monoclonal antibody specific for Pseudomonas
aeruginosa outer membrane protein I
JOURNAL Gene 74 (2), 335-345 (1988)
COMMENT On Nov 28, 1994 this sequence version replaced gi:342017.
MEDLINE 89232725
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/strain="BALB/c"
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/gene="Iqk"
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sig\_peptide  
CDS

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RESULT 2
LOCUS A13733 480 bp DNA PAT 03-JAN-1994
DEFINITION variable region of a monoclonal antibody which cross reacts with 19
known P.aeruginosa serotypes.
ACCESSION A13733
VERSION A13733.1 GI:491741
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 480)
AUTHORS Domdey,H., Margel,M. and von Specht,B.U.
TITLE Monoclonal antibodies to Pseudomonas aeruginosa, their production
and use
JOURNAL Patent: EP 0338395-A 1 25-OCT-1989;
BEHRINGERWERKE Aktiengesellschaft
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source 1..480
/organism="synthetic construct"
/db_xref="taxon:32630"
37..>480
/codon_start=1
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Campus Universitario, Asa Norte, Brasilia, DF 70910-900, Brazil  
Location/Qualifiers  
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/strain="Balb/c"  
/db\_xref="taxon:10090"  
/cell\_line="1H12"  
/cell\_type="hybridoma"  
1. .>419  
/gene="IgK"  
21. .>419  
/gene="IgK"  
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/codon\_start=1  
/product="Immunoglobulin light chain variable region"  
/protein\_id="AAB60862.1"  
/db\_xref="GI:2183077"  
/translation="MDSQAOVILILLVNSCTGDIWVSQSPSSLAVSGAEVYMSK  
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BASE COUNT 105 a 101 c 115 g 98 t  
ORIGIN

Query Match 84.2%; Score 333.6; DB 94; Length 419;  
Best Local Similarity 90.2%; Pred. No. 1.6e-99;  
Matches 357; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

OY 1 atgagattcacagggccaggcttctatatatgtcgtcgtctatgtggtatctggaacctgtgg 60  
DB 21 ATGAGATTCAAGGCCCGAGGTCTTATATTGCTGCTCTATGGGTATGTGATCTGTGG 80  
OY 61 gacattgtctgacacagctccagatcccttgctgtaagcttaagagagagagagccact 120  
DB 81 GACATTGTGATGTCACAGTCTCCATCTCCCTGGCTGTGTACAGCAGAGAGAGTCACT 140  
OY 121 attagctgaatccacagctcagagctgtctcaacagtagaaccgagagaaactacttgct 180  
DB 141 ATGAGCTGCAAGTCCAGTCAAGTCTGCTCAAAAGTAGAACCAGAGAAATTACTTGCT 200  
OY 181 tggtagcagaagaacacagggcagcctcctaaactgtatctactacgtggcatccactaag 240  
DB 201 TGGTACACAGAGCCAGGAGGAGGCTCCCAACTCTATCTACATGCGGATCCATCAGG 260  
OY 241 gaatcgggggtccctatcgcttcagtggaagtgaatcctggagacagattcaactccacc 300  
DB 261 GAATCGGGGTCCCTATGCTTACAGAGCAGTGGATCTGGGACATTTCACTCTCACC 320  
OY 301 atcagcagctcgaagcgtgaagacgtgagcttattactcgaacaaactataactt 360  
DB 321 ATCAGCAGTGTGAGGCTGAAGACCTGGCAATTTATTACTGCAAGCAATCTTATATCTT 380  
OY 361 tacagcttgagacagggagacaaagtgtgaaataaaa 396  
DB 381 CGAGCTTGGTGAGAGGCCCAAGCTGGAATCAAA 416

RESULT 5  
LOCUS A44968 940 bp DNA PAT 07-MAR-1997  
DEFINITION Sequence 24 from Patent W09515382.  
ACCESSION A44968  
VERSION A44968.1 GI:2299554  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.

REFERENCE  
AUTHORS 1 (bases 1 to 940)  
Rose, M.S., Boot, C., Copley, C.G., Paterson, D.S., Hall, S.M.,  
Wright, A.F., and Blakey, D.C.  
TITLE BINDING STRUCTURES DIRECTED AGAINST THE CA55.1 ANTIGEN  
JOURNAL Patent: WO 9515382-A 24 08-JUN-1995;  
ZENECA LTD (GB)

COMMENT Other publication GB 2297751 960814  
Other publication CA 2174972 950608  
Other publication ZA 9409266 950605  
Other publication AU 1113095 950619.  
Location/Qualifiers  
1. .940  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 241 a 266 c 213 g 220 t  
ORIGIN

Query Match 83.8%; Score 332; DB 9; Length 940;  
Best Local Similarity 89.9%; Pred. No. 5.6e-99;  
Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 1 atgagattcacagggccaggcttctatatatgtcgtcgtctatgtggtatctggaacctgtgg 60  
DB 10 ATGAGATTCAAGGCCCGAGGTCTTATATTGCTGCTCTATGGGTATCTGAACTGTGG 69  
OY 61 gacattgtctgacacagctccagatcccttgctgtaagcttaagagagagagccact 120  
DB 70 GACATTGTGATGTCACAGTCTCCATCTCCCTGGCTGTGTACAGCAGAGAGAGTCACT 129  
OY 121 attagctgaatccacagctcagagctgtctcaacagtagaaccgagagaaactacttgct 180  
DB 130 ATGAGCTGCAAAATCCAGTCAAGTCTCTCAACAGTAGAACCAGAAAGAACTACTTGCT 189  
OY 181 tggtagcagaagaacacagggcagcctcctaaactgtatctactacgtggcatccactaag 240  
DB 190 TGGTACACAGAGCCAGGAGGAGGCTCTCTAACTGCTATCTATTGGCATTCACATGAG 249  
OY 241 gaatcgggggtccctatcgcttcagtggaagtgaatcctggagacagattcaactccacc 300  
DB 250 ACATCTGGGGTCCCTATGCTTACAGAGCAGTGGATCTGGGACATTTCACTCTCACC 309  
OY 301 atcagcagctcgaagcgtgaagacgtgagcttattactcgaacaaactataactt 360  
DB 310 ATCAGCAGTGTGAGGCTGAAGACCTGGCAATTTATTACTGCAAGCAATCTTATCTT 369  
OY 361 tacagcttgagacagggagacaaagtgtgaaataaaa 396  
DB 370 CGAGCTTGGTGAGAGGCCCAAGCTGGAATCAAA 405

RESULT 6  
LOCUS I64459 940 bp DNA PAT 07-OCT-1997  
DEFINITION Sequence 24 from patent US 5665357.  
ACCESSION I64459  
VERSION I64459.1 GI:2481353  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 940)  
Rose, M.S., Boot, C., Copley, C.G., Paterson, D.S., Hall, S.M.,  
Wright, A.F., and Blakey, D.C.  
TITLE Antibodies recognizing tumor associated antigen CA 55.1  
JOURNAL Patent: US 5665357-A 24 09-SEP-1997;  
FEATURES Location/Qualifiers  
1. .940  
/organism="unknown"  
BASE COUNT 241 a 266 c 213 g 220 t  
ORIGIN

Query Match 83.8%; Score 332; DB 10; Length 940;  
Best Local Similarity 89.9%; Pred. No. 5.6e-99;  
Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 1 atgagattcacagggccaggcttctatatatgtcgtcgtctatgtggtatctggaacctgtgg 60  
DB 11 ATGAGATTCAAGGCCCGAGGTCTTATATTGCTGCTCTATGGGTATCTGAACTGTGG 69

Db 20 ATGATTCACAGAGCCAGGCTTCTTATTCGTCTGCTATGAGTATCTGAACTGTGGG 69  
OY 61 gacattgacggaacacatctccagatccctgctgtaagcttagagagagggccact 120  
Db 70 GACATTGATGATGTCACAGCTTCATCTCCCTGGCTGTGTACAGCAGAGAGAGAGGTTACT 129  
OY 121 attagctcaaatccagtcagagctgctcaacagtagaaccggagaacactctgct 180  
Db 130 ATGAGCTCAATCCAGTCAGAGCTCTCTCAACACTAGAACCCGAAAGAACTACTGGCT 189  
OY 181 tggtaaccagagaacccagggagcagctccctaaactgctgatactactgagcactag 240  
Db 190 TGGTACACGACGAGACAGGAGGAGCTCTTAACCTGATGATCTATTGGGCACTCAGG 249  
OY 241 gaattgggtccctgagctcagctcagctgagctgagctgagagagattcaactcacc 300  
Db 250 ACATCTGGGGTCCCTGATCTGCTTACAGAGCAGTGGATCTGGGACAGATTTCCTCTCAC 309  
OY 301 atcagcagctcagcagcagcagcagcagcttactactgacagcaactctataact 360  
Db 310 ATCAGCAGCTGTGACAGCTGAGAGACCTGGCAATTTTACTGTGACCAATCTTACTCT 369  
OY 361 tacacgttcgacagcagggagcgaagtggagaataaa 396  
Db 370 CGGAGCTTCGGTGGAGGACCAAGCTGGAATCAAA 405

## RESULT 7

LOCUS MMLA21LEV 401 bp DNA ROD 15-JUN-1993  
DEFINITION M.musculus DNA for Ige antibody light chain (VJ).  
ACCESSION X65774  
VERSION X65774.1 GI:312076  
KEYWORDS Ige antibody; J-segment; light chain; V-region.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 401)  
Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Kotler, H., Schneeg, I., Geley, S., Helmsberg, A., Varga, J.M. and Kotler, R.

TITLE Mechanism of allergic cross-reactions--III. cDNA cloning and variable-region sequence analysis of two Ige antibodies specific for trinitrophenyl

JOURNAL Mol. Immunol. 29 (2), 161-166 (1992)

FEATURES 92178225

source Location/Qualifiers

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/db\_xref="taxon:10090"  
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/codon\_start=1  
/product="Ige antibody light chain (VJ)"  
/protein\_id="CAA4658.1"  
/db\_xref="GI:312076"

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SSQSLVSSNKNLANTOKRPGSPKLIYMASTRSGVDRFTGSGSGIDFTLLTIS  
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V.region  
/product="Ige antibody light chain (VJ)"  
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BASE COUNT 100 a 91 c 105 g 105 t

ORIGIN

Query Match 76.1%; Score 301.4; DB 94; Length 401;  
Best Local Similarity 86.5%; Pred. No. 7.6e-89;

Matches 345; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

OY 1 atgattacagcagcagcttctatctgctcgtctatggtatctgacacctgtggg 60  
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Db 3 ATGATTCACAGAGCCAGGCTTCTTATTCGTCTGCTATGAGTATCTGAACTGTGGG 62  
OY 61 gacattgacggaacacatctccagatccctgctgtaagcttagagagagggccact 120  
Db 63 GACATTGATGATGTCACAGCTTCATCTCCCTGGCTGTGTACAGCAGAGAGAGAGGTTACT 122  
OY 121 attagctcaaatccagtcagagctgctcaacagtagaaccggagaacactctgct 180  
Db 123 ATGAGCTCAATCCAGTCAGAGCTCTCTCAACACTAGAACCCGAAAGAACTACTGGCT 182  
OY 181 tggtaaccagagaacccagggagcagctccctaaactgctgatactactgagcactag 240  
Db 183 TGGTACACGACGAGACAGGAGGAGCTCTTAACCTGATGATCTATTGGGCACTCAGG 242  
OY 241 gaattgggtccctgagctcagctcagctgagctgagctgagagagattcaactcacc 300  
Db 243 GAATCTGGGGTCCCTGATCTGCTTACAGAGCAGTGGATCTGGGACAGATTTCCTCTCAC 302  
OY 301 atcagcagctcagcagcagcagcagcagcttactactgacagcaactctataact 357  
Db 303 ATCAGCAGCTGTGACAGCTGAGAGACCTGGCAATTTTACTGTGACCAATCTTACTCT 362  
OY 361 tacacgttcgacagcagggagcgaagtggagaataaa 396  
Db 363 CCGTACAGCTTCGGTGGAGGACCAAGCTGGAATCAAA 401

## RESULT 8

LOCUS MUSIGKALA 402 bp mRNA ROD 14-JUL-1993  
DEFINITION Mouse Ig rearranged K-chain mRNA V-region, 5' end.  
ACCESSION M98042  
VERSION M98042.1 GI:196749  
KEYWORDS V-region; hepatitis; immunoglobulin light chain; processed gene.  
SOURCE Mus musculus (strain BALB/c, sub-species domesticus) spleen cDNA to mRNA.

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 402)  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Hong, H.J., Kim, A.K., Ryu, C.J., Park, S.S., Chung, H.K., Kwon, K.S., Kim, K.L., Kim, J. and Han, M.

TITLE Cloning and characterization of cDNA's coding for heavy and light chains of a monoclonal antibody specific for pre-S2 antigen of hepatitis B virus

JOURNAL Gene 121, 331-335 (1992)

FEATURES 93077049

source Location/Qualifiers

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/partial  
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/function="specific for pre-S2 antigen of hepatitis B virus"

BASE COUNT 102 a 93 c 100 g 107 t

ORIGIN

Query Match 61.4%; Score 102.4; DB 94; Length 402;  
Best Local Similarity 51.5%; Pred. No. 1.2e-89;

Matches 345; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

OY 1 atgattacagcagcagcttctatctgctcgtctatggtatctgacacctgtggg 60  
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Query Match. 75.3%; Score 298.2; DB 94; Length 402;  
 Best Local Similarity 86.0%; Pred. No. 8.7e-88;  
 Matches 343; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

OY 1 atggaattacagagccaggtcttatatctgctgctcattggtatctggaacctgtgg 60  
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 Db 1 ATGGATTACAGAGCCAGGTTCTTATGTTACTGCTGATGGTATGTTGACCTGTGG 60  
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OY 61 gacattgtcgtcagacagctccagatccctgctgctgaagcttagagagagggccact 120  
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 Db 61 GACATTGTGANTGCACAGTCTCCATCTCCCTAGCTGTGTAGTTGGAGAGAGTTACT 120  
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OY 121 attagctcaaatccagtcagagctgtctcaacagtagaacccgagagaactactgtgct 180  
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 Db 121 ATGACCTGCAATCCAGTCAGAGCCTTTTATATATAGTACATTCAAAAGAACTACTGGCC 180  
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OY 121 atgacttcgaatccagtcagagctgtctcaacagtagaacccgagagaactactgtgct 180  
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OY 181 tggtaaccagcaagaaccagggagccctcctaactgctgactactggtgcatccactagg 240  
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 Db 181 TGGTACCAAGCAAGAAACAGGAGCAGTCTCTAAACTGTGATTACTGGCATCCACTAGG 240  
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OY 241 gaacttgagggtccctgactgactgctgagtgagtgatctggagacagattcactctacc 300  
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 Db 241 GAATCTGGGGTCCCTGATCGCTTCACAGCAGTGATGTGAGACAGATTTCACCTCCACC 300  
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OY 301 atcagcagctgcagagctggaagagctgtgacgtttactgcaagcaactctata---at 357  
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 Db 301 ATCAGCATGTGTAAGGCTGGAAGACCTGGCAGTTTATTTACTGTCAGACATATTATATACATAT 360  
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OY 358 cttaacacgttcgagcagagggagcaagtggaataaata 396  
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 Db 361 CCGTCCACGTTCCGAGGGGAGGACCTACTCGAATAATAA 399  
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RESULT 9  
 AF163745 336 bp mRNA ROD 04-AUG-1999  
 LOCUS Mus musculus mab 27.4.1 immunoglobulin light chain variable region  
 DEFINITION AF163745  
 ACCESSION AF163745  
 VERSION AF163745.1 GI:5690296  
 KEYWORDS  
 ORGANISM house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 336)  
 AUTHORS Mertens,N.M., Galvin,J.E., Adderson,E.E. and Cunningham,M.W.  
 TITLE Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal  
 Mouse Monoclonal Antibodies  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 336)  
 AUTHORS Mertens,N.M. and Cunningham,M.W.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma  
 University Health Sciences Center, 940 St. Young Blvd, Oklahoma  
 City, OK 73190, USA  
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 /note="mab 27.4.1"  
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 /product="immunoglobulin light chain variable region"  
 /protein\_id="AADA7024.1"  
 /db\_xref="GI:5690297"  
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 KPGSGPKLIYMASTRRESGVDRFTGSGSDFTLTISSVQAEELAVYYCKOSINLYT  
 FGGGTKEIKR"  
 CDS  
 BASE COUNT 91 a 83 c 86 g 76 t

ORIGIN

Query Match. 74.7%; Score 296; DB 94; Length 336;  
 Best Local Similarity 92.6%; Pred. No. 4.7e-87;  
 Matches 311; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 61 gacattgtcgtcagacagctccagatccctgctgctgaagcttagagagagggccact 120  
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 Db 1 GACATTGTGANTGCACAGTCTCCATCTCCCTGCTGTGACAGAGAGAGAGTACT 60  
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OY 121 attagctcaaatccagtcagagctgtctcaacagtagaacccgagagaactactgtgct 180  
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 Db 61 ATGAGCTGCAATCCAGTCAGAGCCTCTCAACAGTGAACCCGAAAGAACTACTGGCT 120  
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OY 181 tggtaaccagcaagaaccagggagccctcctaactgctgactactggtgcatccactagg 240  
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 Db 121 TGGTACCAAGCAAGAAACAGGAGCAGTCTCTAAACTGTGATTACTGGCATCCACTAGG 180  
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OY 241 gaacttgagggtccctgactgactgctgagtgagtgatctggagacagattcactctacc 300  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 181 GAATCTGGGGTCCCTGATCGCTTCACAGCAGTGATGTGAGACAGATTTCACCTCCACC 240  
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OY 301 atcagcagctgcagagctggaagagctgtgacgtttactgcaagcaactctataactct 360  
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 Db 241 ATCAGCATGTGTAAGGCTGGAAGACCTGGCAGTTTATTTACTGTCAGACATATTATATACATAT 300  
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OY 361 tacacgttcgagcagagggagaccaagtgaataaata 396  
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 Db 301 TACACGTTCCGAGGGGAGGACCAAGCTGGAATAATAA 336  
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RESULT 10  
 MDIGKVAR 336 bp mRNA ROD 05-NOV-1994  
 LOCUS M.domesticus igk variable region.  
 DEFINITION 222063.1 GI:297629  
 ACCESSION 222063.1 GI:297629  
 VERSION anti-DNA antibody; Igk gene; igk variable region; immunoglobulin.  
 KEYWORDS western European house mouse.  
 ORGANISM Mus musculus domesticus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Euteleostomi;  
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 336)  
 AUTHORS Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.  
 TITLE Both IgM and IgG anti-DNA antibodies are the products of clonally  
 selective B cell stimulation in (NZB x NZM)F1 mice  
 JOURNAL J. Exp. Med. 176 (3), 761-779 (1992)  
 MEDLINE 92381444  
 REFERENCE 2 (bases 1 to 336)  
 AUTHORS Marion,T.N.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-MAR-1993) Tony N. Marion, Microbiology and  
 Immunology, University of Tennessee, Memphis, 858 Madison Avenue,  
 Memphis, TN, 38163, USA  
 FEATURES  
 source location/Qualifiers  
 1. 336  
 /organism="Mus musculus domesticus"  
 /strain="(NZB x NZM)F1"  
 /isolate="mouse #165"  
 /db\_xref="taxon:10092"  
 /chromosome="6"  
 /sex="Female"  
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 /tissue\_type="spleen"  
 /cell\_type="hybridoma"  
 /cell\_line="165.45"  
 1. 336  
 /gene="Igk"  
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 antibody; Vx8 family"

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/codon_start=1
/product="immunoglobulin variable region"
/protein_id="CA80037.1"
/db_xref="GI:297630"
/translation="DIVMSQSPSSLAWSAGEKVTMSCKSSQSLNSRTRKLYLWYQO
KPGQSPKLIYMASTRESGVPDRFTGSQSGDFTLTSSVQAEIDLAVYYCKOSYNLVT
FGGSKLEIK"

BASE COUNT      91 a      83 c      86 g      76 t
ORIGIN

Query Match      74.7%; Score 296; DB 94; Length 336;
Best Local Similarity 92.6%; Pred. No. 4.7e-87;
Matches 311; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 61 gacattgctgacacagctccagatccctgctgctgtaagcttagagagagccact 120
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DB 1 GACATTGTGATGTCACAGTCTCCATCTCCCTGCTGCTGCAGCAGAGAGAGTCACT 60
OY 121 attagctgaatccagtcagatgctgtctcaacagtagaacccggagagacttgct 180
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 61 ATGACTGCAATCCAGTCAGAGTCTCTCAACAGTAGAACCCGAAAGACTTGGCT 120
OY 181 tggtaaccagcagaaccaggcagcctcctaaactgctgctatctatctgagcactag 240
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 121 TGGTACACAGCAAAACAGGCGCATCTCTTAACGTGATCTACTGGGCATCCACTAG 180
OY 241 gaattggggtccctgctgctcagtgagtgagtgatctggagacattcactcacc 300
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DB 181 GAATCTGGGGTCCCTGATGCTTTCACAGCGCATGATCGGACAGATTCTCACTCCACC 240
OY 301 atccagcagctcagcagcgtgaagcgtgcaagtcttactgacccaattctatctt 360
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DB 241 ATCAGCAGTGTCTCAGGCTGAAGACCTGGCAGTTTATTAATCTGCAAGCAATCTTATATCTG 300
OY 361 tacacgttcgacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 396
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DB 301 TACAGCTTCGAGGGGGGACCAAGCTGGAAATATAA 336

RESULT 11
AB028876      339 bp      mRNA      ROD      07-DEC-1999
LOCUS      Mus musculus mRNA for 5.2 Igg light chain (variable region),
DEFINITION      partial cds.
ACCESSION      AB028876
VERSION      AB028876.1 GI:5103290
KEYWORDS      5.2 Igg light chain variable region.
SOURCE      Mus musculus cell_line:hybridoma 5.2 cDNA to mRNA.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      Yoshida,S., Matsuo,K., Luo,D., Iwai,K., Arai,M., Sinden,R.E. and
AUTHORS      Ishii,A.
TITLE      A single-chain antibody fragment specific for the Plasmodium
beigheii ookinete protein Pbs21 confers transmission blockade in the
mosquito midgut
Mol. Biochem. Parasitol. 104 (2), 195-204 (1999)
JOURNAL      MEDLINE
REFERENCE      20058748
AUTHORS      2 (bases 1 to 339)
TITLE      Yoshida,S.
Direct Submission
Submitted (11-JUN-1999) to the DDBJ/EMBL/GenBank databases. Shigeto
Yoshida, Jichi Medical School, Department of Medical Zoology;
Yakushiji 3311-1, Minamikawachimachi, Tochigi 329-0498, Japan
(E-mail:shigeto@jichi.ac.jp, Tel:81-285-58-7339,
Fax:81-285-44-6489)
FEATURES
Source      Location/Qualifiers
1..339
/db_xref="taxon:10090"
/cell_line="hybridoma 5.2"
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BASE COUNT      92 a      84 c      87 g      76 t
ORIGIN

Query Match      74.7%; Score 296; DB 94; Length 339;
Best Local Similarity 92.6%; Pred. No. 4.7e-87;
Matches 311; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 61 gacattgctgacacagctccagatccctgctgctgtaagcttagagagagccact 120
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DB 1 GACATTGTGATGTCACAGTCTCCATCTCCCTGCTGCTGCAGCAGAGAGAGTCACT 60
OY 121 attagctgaatccagtcagatgctgtctcaacagtagaacccggagagacttgct 180
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DB 61 ATGACTGCAATCCAGTCAGAGTCTCTCAACAGTAGAACCCGAAAGACTTGGCT 120
OY 181 tggtaaccagcagaaccaggcagcctcctaaactgctgctatctatctgagcactag 240
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DB 121 TGGTACACAGCAAAACAGGCGCATCTCTTAACGTGATCTACTGGGCATCCACTAG 180
OY 241 gaattggggtccctgctgctcagtgagtgagtgatctggagacattcactcacc 300
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DB 181 GAATCTGGGGTCCCTGATGCTTTCACAGCGCATGATCGGACAGATTCTCACTCCACC 240
OY 301 atccagcagctcagcagcgtgaagcgtgcaagtcttactgacccaattctatctt 360
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DB 241 ATCAGCAGTGTCTCAGGCTGAAGACCTGGCAGTTTATTAATCTGCAAGCAATCTTATATCTG 300
OY 361 tacacgttcgacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 396
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 301 TACAGCTTCGAGGGGGGACCAAGCTGGAAATATAA 336

RESULT 12
S81289      408 bp      mRNA      ROD      23-MAY-1996
LOCUS      Igm kappa chain variable region [CDR1 to CDR3 region] [rats, LEW,
DEFINITION      HAR-1 hybridoma cells, mRNA Partial, 408 nt].
ACCESSION      S81289
VERSION      S81289.1 GI:1326409
KEYWORDS
SOURCE      Rattus sp. LEW HAR-1 hybridoma cells.
ORGANISM      Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE      Bortle,D.C., Cramer,D.V., Shirvan,H., Wu,G.D., Rodriguez,O.,
AUTHORS      Chapman,F.A. and Makowka,L.
TITLE      Genetic control of the humoral immune response to xenografts. II.
Monoclonal antibodies that cause rejection of heart xenografts are
encoded by germ-line immunoglobulin genes
Transplantation 60 (12), 1504-1510 (1995)
JOURNAL      MEDLINE
REMARK      96125839
GenBank staff at the National Library of Medicine created this
entry [NCBI gisbq 176405] from the original journal article.
This sequence comes from Fig. 4.
FEATURES
Source      Location/Qualifiers
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CDS
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7..408
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/gene="igm kappa chain variable region"
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/partial
/gene="igm kappa chain variable region"
/note="hamster heart xenograft rejection-associated; ;
This sequence comes from Fig. 4"
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/protein_id="AAB35891.1"
/db_xref="GI:1326410"
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SVQEDDAVYICQOQYINITYTGACTKEIKNA"
BASE COUNT      106 a      100 c      108 g      94 t
ORIGIN

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Query Match	74.58;	Score 295.2;	DB 95;	Length 408;
Best Local Similarity	84.18;	Pred. No. 8.6e-87;		
Matches 333; Conservative	0;	Mismatches 63;	Indels 0;	Gaps 0;

Oy	1	atgattcaacagggccaggtctctatatcttgctgctgtatggatctggtatctggtaccctgtagg	60
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Oy	61	gacattctgctgcagacagctctccagatctccctgctgctgaaagcttagagagagagggccact	120
Db	67	gacatttggtgatggaccacagctccatccctccagcctgtgtgcagaggagagaggtacct	126
Oy	121	attagctgcaaaatccagtcagagctctgctctcaacagtagaacccgagagaaactcttgct	180
Db	127	atgaccttcacagctccagctcacagctcttttatcatcattaaaaacaaaaaagactacttgccc	186
Oy	181	tgtttcccgacgaaacccgagggcagctccctcaaacctgtctgttctactgtggtaccactagg	240
Db	187	tgtgttccacgcaaaacccagggcactgtcttcttaactgctgtatctggtggatccactagg	246
Oy	241	gaattctggtgtccctctgatactgcttcaagtgtgacgttgagatctctggacagaatttcactctaac	300
Db	247	gaattctggtgtccctctgatactgcttcaagtgtgacgttgagatctctggacagaatttcactctaac	306
Oy	301	atccagcagctctgcagagctgtaagacgttgagcttattactctgacgcgaattctataaactt	360
Db	307	atccagcagctctgcagagcaggaagacctgtgcttttattactgtccacgacagctattacttg	366
Oy	361	tacagcttctgcagcaggtggaacaaagtgaataaataa	396
Db	367	tacagcttctgcagcaggtggaacaaacctggaactgaaa	402

RESULT	13
MUSIGKV130	
LOCUS	MUSIGKV130
DEFINITION	Mus musculus Ig rearrange kappa-chain gene V19-J1 region.
ACCESSION	L16819
VERSION	L16819.1
KEYWORDS	GI:293622
SOURCE	V-region; complementarity determining region; immunoglobulin light chain; kappa-immunoglobulin; processed gene.
ORGANISM	Mus musculus (strain NZB/W F1) mRNA.
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 339) Lustgarten,D.L., Kavalier,J., Gerhard,W. and Scharff,M.D. The response to a foreign antigen in the autoimmune NZB/W F1 murine strain Unpublished (1993)
JOURNAL	Location/Oallifiers
FEATURES	1..339
source	/organism="Mus musculus"

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265..291
/gene="Igf-V19"
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286..324
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misc_feature
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J_segment
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BASE COUNT      89 a | 85 c   88 g   76 t   1 others
ORIGIN
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Query Match	95.5%	Score	295	DB	94	Length	339
Best Local Similarity	92.3%	Pred	No.	1e-86			
Matches	310	Conservative	0	Mismatches	26	Indels	0
						Gaps	0

OY	61	gaatctgctcgaaacaaatctccagaattccctggctctgaaattgagagaaagagccat	120
Db	1	GACATTGTGATGTACAGCTCTCCATCTCTCCCTGGCTGTGTACAGAGAGAGGGTACT	60
OY	121	attagctgcnaatccagctcaagctctgctctcaacagtagaaccgagagaactactgct	180
Db	61	ATGACTCTCAATATCCAGTCACAGCTCTGCTCAACAGTAGAACCCCAAGAACTACTTGGCT	120
OY	181	tgtatccagcagaacccagggcagcctctccaaactgtctgatactcactgagatccactag	240
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OY	241	gaatctgggtctccatgactcgtctcaatgtagcagtgagatctggagacagatltcaactcaac	300
Db	181	GAATCTGGGGTCCCTCGAATCGGCTTACACAGGCGATGGATCTGGGACAGATTCACCTTCACC	240
OY	301	atcagcagcttcgcagagctcgtgaagaacgttgcgaattatattacagcaacgcacattataatct	360
Db	241	ATCAGCACTGTGCAGAGCGCTGAGACCTGGCACTTATTATCTGCAACGAATCTTAAATCCT	300
OY	361	tacacgtctcgacagagggagccaaagtgtgaaataaa	396
Db	301	TACAGCTTCGGAGGGGAGCACAACCTGGAATAATAAA	336

RESULT 14			
MIDGVAI			
LOCUS	MIDGVAI	336 bp	mRNA
DEFINITION	M.domesticus Igg variable region.		
ACCESSION	222039		ROD
VERSION	222039.1	GI:297576	
KEYWORDS	anti-DNA antibody; IgG gene; IgG variable region; Immunoglobulin.		
SOURCE	western European house mouse.		
ORGANISM	Mus musculus domesticus		
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
	Rodentia; Sciurognath; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 336)		
AUTHORS	Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.		
TITLE	Both IgM and IgG anti-DNA antibodies are the products of clonally		
	selective B cell stimulation in (NZB x NZW)F1 mice		
JOURNAL	J. Exp. Med.	176 (3),	761-779 (1992)
MEDLINE	9238144		
REFERENCE	2 (bases 1 to 336)		
AUTHORS	Marion,T.N.		



TITLE Direct Submission  
JOURNAL Submitted (23-MAR-1993) Tony N. Marion, Microbiology and Immunology, University of Tennessee, Memphis, 858 Madison Avenue, Memphis, TN 38163, USA

## FEATURES

source Location/Qualifiers

1.336  
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ORIGIN

Query Match 73.9%; Score 292.8; DB 94; Length 336;  
Best Local Similarity 92.0%; Pred. No. 5.4e-86;  
Matches 309; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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DB 1 GACATGTGTGATGTACAGATCTCCATCTCCCTGCTGTGTCAGAGAGAGAGTCACT 60  
QY 121 attagctgcaaatccagctcagctgctcctcaacagtagaacccgagagaaacttggct 180  
DB 61 ATGAGCTGCAAAATCCAGTCAAGTCTCTCAACAGTAGAAACCGAAAGAACTACTTGGCT 120  
QY 181 tggtaaccagcaagaacagagcagcctccctaaactgctgactgactgagcactcactagg 240  
DB 121 TGGTACCAAGCAAGAACCAAGGCACTCTTAACCTGCTGATCTACTGGGCATCCAGTAGG 180  
QY 241 gaactggtggtccctgactcgtctcagctgagctgagctgagacagattcactcacc 300  
DB 181 GAATCTGGGGTCCCTGATGCTTCAACAGCGAGTGATCTGGGAGATTTCACTCTCAACC 240  
QY 301 atcagcagctgctcagctgagagcgttgagcagttatctactcagcagcaacttataactt 360  
DB 241 ATCAGCACTGTGACAGCTGAGAGACCTGGCAGTTATTACTCAAGCAATCTTATAATCTG 300  
QY 361 tacacgttcgacacagggagaccagagtggaataaaa 396  
DB 301 TACACGTTTCGGGGGGGGGACCAAGCTGGAATATAAA 336

RESULT 15  
LOCUS MDIGKVAU 336 bp mRNA  
DEFINITION M.domesticus Igc variable region.  
ACCESSION 222070  
VERSION 222070.1 GI:297635  
KEYWORDS anti-DNA antibody; Igc gene; Igc variable region; immunoglobulin.  
SOURCE western European house mouse.

## ORGANISM

Mus musculus domesticus  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 336)  
Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.  
Both Igm and Igc anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice  
J. Exp. Med. 176 (3), 761-779 (1992)

## JOURNAL

## MEDLINE

## 9238144

## REFERENCE

## 2 (bases 1 to 336)

## MARION,T.N.

## TITLE

## Direct Submission

## JOURNAL

## Submitted (23-MAR-1993) Tony N. Marion, Microbiology and Immunology, University of Tennessee, Memphis, 858 Madison Avenue, Memphis, TN 38163, USA

## FEATURES

## source Location/Qualifiers

1.336  
/organism="Mus musculus domesticus"  
/strain="(NZB x NZW)F1"  
/isolate="mouse #165"  
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BASE COUNT 91 a 83 c 86 g 76 t  
ORIGIN

Query Match 73.9%; Score 292.8; DB 94; Length 336;  
Best Local Similarity 92.0%; Pred. No. 5.4e-86;  
Matches 309; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 61 gacatgtgctgacacagctccagatccctgctgtaagcttagagagagagccact 120  
DB 1 GACATGTGTGATGTACAGATCTCCATCTCCCTGCTGTGTCAGAGAGAGAGTCACT 60  
QY 121 attagctgcaaatccagctcagctgctcctcaacagtagaacccgagagaaacttggct 180  
DB 61 ATGAGCTGCAAAATCCAGTCAAGTCTCTCAACAGTAGAAACCGAAAGAACTACTTGGCT 120  
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DB 121 TGGTACCAAGCAAGAACCAAGGCACTCTTAACCTGCTGATCTACTGGGCATCCAGTAGG 180  
QY 241 gaactggtggtccctgactcgtctcagctgagctgagctgagacagattcactcacc 300  
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QY 301 atcagcagctgctcagctgagagcgttgagcagttatctactcagcagcaacttataactt 360  
DB 301 ATCAGCACTGTGACAGCTGAGAGACCTGGCAGTTATTACTCAAGCAATCTTATAATCTG 300  
QY 361 tacacgttcgacacagggagaccagagtggaataaaa 396  
DB 301 TACACGTTTCGGGGGGGGGACCAAGCTGGAATATAAA 336

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Job time: 5614 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 20:11:00 ; Search time 1635.84 seconds  
(without alignments)  
35.383 Million cell updates/sec

Title: US-09-249-011-7  
396

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Gapop 10.0 , Gapext 1.0

Searched: 9623517 segs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
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18: gb\_est18:\*  
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21: gb\_est21:\*  
22: gb\_est22:\*  
23: gb\_est23:\*  
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25: gb\_est25:\*  
26: gb\_est26:\*  
27: gb\_est27:\*  
28: gb\_est28:\*  
29: gb\_est29:\*  
30: gb\_est30:\*  
31: gb\_est31:\*  
32: gb\_est32:\*  
33: gb\_est33:\*  
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36: gb\_est36:\*  
37: gb\_est37:\*  
38: gb\_est38:\*  
39: gb\_est39:\*  
40: gb\_est40:\*  
41: gb\_est41:\*  
42: gb\_est42:\*  
43: gb\_est43:\*

44: em\_esthum10:\*  
45: em\_esthum11:\*  
46: em\_esthum12:\*  
47: em\_esthum13:\*  
48: em\_esthum14:\*  
49: em\_esthum15:\*  
50: em\_esthum16:\*  
51: em\_esthum17:\*  
52: em\_esthum18:\*  
53: em\_esthum19:\*  
54: em\_esthum20:\*  
55: em\_esthum21:\*  
56: em\_esthum22:\*  
57: em\_esthum23:\*  
58: em\_esthum24:\*  
59: em\_esthum25:\*  
60: em\_esthum26:\*  
61: em\_esthum27:\*  
62: em\_esthum28:\*  
63: em\_esthum29:\*  
64: em\_esthum30:\*  
65: em\_esthum31:\*  
66: em\_esthum32:\*  
67: em\_esthum33:\*  
68: em\_esthum34:\*  
69: em\_esthum35:\*  
70: em\_esthum36:\*  
71: em\_esthum37:\*  
72: em\_esthum38:\*  
73: em\_esthum39:\*  
74: em\_esthum40:\*  
75: em\_esthum41:\*  
76: em\_esthum42:\*  
77: em\_esthum43:\*  
78: em\_esthum44:\*  
79: em\_esthum45:\*  
80: em\_esthum46:\*  
81: em\_esthum47:\*  
82: em\_esthum48:\*  
83: em\_esthum49:\*  
84: em\_esthum50:\*  
85: em\_esthum51:\*  
86: em\_esthum52:\*  
87: em\_esthum53:\*  
88: em\_esthum54:\*  
89: em\_esthum55:\*  
90: em\_esthum56:\*  
91: em\_esthum57:\*  
92: em\_esthum58:\*  
93: em\_esthum59:\*  
94: em\_esthum60:\*  
95: em\_esthum61:\*  
96: em\_esthum62:\*  
97: em\_esthum63:\*  
98: em\_esthum64:\*  
99: em\_esthum65:\*  
100: em\_esthum66:\*  
101: em\_esthum67:\*  
102: em\_esthum68:\*  
103: em\_esthum69:\*  
104: em\_esthum70:\*  
105: em\_esthum71:\*  
106: em\_esthum72:\*  
107: em\_esthum73:\*  
108: em\_esthum74:\*  
109: em\_esthum75:\*  
110: em\_esthum76:\*  
111: em\_esthum77:\*  
112: em\_esthum78:\*  
113: em\_esthum79:\*  
114: em\_esthum80:\*  
115: em\_esthum81:\*  
116: em\_esthum82:\*

117: gb\_est48:\*  
 118: gb\_est49:\*  
 119: gb\_est50:\*  
 120: gb\_est51:\*  
 121: gb\_est52:\*  
 122: gb\_est53:\*  
 123: gb\_est54:\*  
 124: gb\_est55:\*  
 125: gb\_est56:\*  
 126: gb\_est57:\*  
 127: gb\_est58:\*  
 128: gb\_est59:\*  
 129: gb\_est60:\*  
 130: gb\_est61:\*  
 131: gb\_est62:\*  
 132: gb\_est63:\*  
 133: gb\_est64:\*  
 134: gb\_est65:\*  
 135: gb\_est66:\*  
 136: gb\_est67:\*  
 137: gb\_est68:\*  
 138: gb\_est69:\*  
 139: gb\_est70:\*  
 140: gb\_est71:\*  
 141: gb\_est72:\*  
 142: gb\_est73:\*  
 143: gb\_est74:\*  
 144: gb\_est75:\*  
 145: gb\_est76:\*  
 146: gb\_est77:\*  
 147: gb\_est78:\*  
 148: gb\_est79:\*  
 149: gb\_est80:\*  
 150: gb\_est81:\*  
 151: gb\_est82:\*  
 152: gb\_est83:\*  
 153: gb\_est84:\*  
 154: gb\_est85:\*  
 155: gb\_est86:\*  
 156: gb\_est87:\*  
 157: gb\_est88:\*  
 158: gb\_est89:\*  
 159: gb\_est90:\*  
 160: gb\_est91:\*  
 161: gb\_est92:\*  
 162: gb\_est93:\*  
 163: gb\_est94:\*  
 164: gb\_est95:\*  
 165: gb\_est96:\*  
 166: gb\_est97:\*  
 167: gb\_est98:\*  
 168: gb\_est99:\*  
 169: gb\_est100:\*  
 170: gb\_est101:\*  
 171: gb\_est102:\*  
 172: gb\_est103:\*  
 173: gb\_est104:\*  
 174: gb\_est105:\*  
 175: gb\_est106:\*  
 176: gb\_est107:\*  
 177: gb\_est108:\*  
 178: gb\_est109:\*  
 179: gb\_est110:\*  
 180: gb\_est111:\*  
 181: gb\_est112:\*  
 182: gb\_est113:\*  
 183: gb\_est114:\*  
 184: gb\_est115:\*  
 185: gb\_est116:\*  
 186: gb\_est117:\*  
 187: gb\_est118:\*  
 188: gb\_est119:\*  
 189: gb\_est120:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Match Length	ID	Description
1	312	78.8	905	BF580037
2	272.8	68.9	691	BF128999
3	258.6	65.3	300	BF148633
4	256	64.6	641	AW405821
5	253.4	64.0	643	AW390282
6	251	63.4	886	BF674779
7	247.6	62.5	508	AW406572
8	244	61.6	388	BF63188
9	240.6	60.8	573	AW951579
10	231.4	58.4	887	BF128857
11	229.6	57.7	401	BF128857
12	228.4	57.0	533	AW802126
13	228.4	57.4	558	BF964753
14	227.2	57.2	503	BF830413
15	226.6	57.1	550	AW404610
16	226.2	57.1	403	AV734428
17	224.6	56.7	630	AW734428
18			114	AW406512

19 221.8 56.0 444 168 BF746228  
20 221.8 56.0 444 168 BF746298  
21 221.6 56.0 397 168 BF746298  
22 220.8 55.8 328 114 AM406484  
23 220.4 55.7 847 151 BF678476  
24 219.8 55.5 635 31 AV702633  
25 219.4 55.4 553 170 BF870122  
26 217.8 55.0 363 5 AA300651  
27 215.2 54.3 364 156 BF72579  
28 201.2 50.8 349 122 AM947280  
29 200 50.5 459 114 AM383565  
30 198.2 50.1 410 172 BG059215  
31 194.2 49.0 333 115 AM407858  
32 190.2 48.0 425 2 A1734035  
33 190.2 48.0 442 7 AA405415  
34 188.4 47.6 423 115 AM406796  
35 187 47.2 594 165 BF309592  
36 187 47.2 597 170 BF868788  
37 185.2 46.8 480 170 BF877467  
38 183.2 46.3 1153 151 BF663521  
39 182.2 46.0 488 114 AM405725  
40 181.8 45.9 445 114 AM405178  
41 181.8 45.9 488 153 H25625  
42 181 45.7 363 7 AA464313  
43 180.6 45.6 454 115 AM406883  
44 180.2 45.5 409 138 BE719012  
45 179.8 45.4 504 114 AM405787

## ALIGNMENTS

RESULT 1  
LOCUS BF580037 905 bp mRNA  
DEFINITION 602095235F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4209417 5',  
mRNA sequence.  
ACCESSION BF580037  
VERSION BF580037.1 GI:11653749  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS 1 (bases 1 to 905)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

FEATURES  
source High quality sequence stop: 757.  
Location/Qualifiers  
1. 905  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4209417"  
/clone\_lib="NCI\_CGAP\_Co24"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: colon; Vector: PCWV-SPOF6; Site:1; Notti:  
Site:2; Sali; Cloned unidirectionally. primer: Oligo dt.  
Average insert size 1.6 kb. constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 248 a 236 c 217 g 204 t

## ORIGIN

## Query Match

Best Local Similarity 78.8%; Score 312.; DB 150; Length 905;  
Matches 363; Conservatave 0; Mismatches 30; Indels 3; Gaps 3;

QY 1 atgattcacagagccaggtttctatatctgctgtatggatctggcacttggg 60  
DB 18 ATGATTACAGAGCCAGGTTCTTATA-TGCTGTGCTAAGGATCTGCTGTGGG 76  
QY 61 gacattgtctgacagcagcttccagattccctgctgtaagcttaagagagagccact 120  
DB 77 GACA-TGTGATGTACACAGTCTCCATCTCTCGGCTGTACACAGAGAGAGATCACT 135  
QY 121 attagctgaatccatccatgagcttctcttaacagatgaaccgagagacttggct 180  
DB 136 ATGAACCTGCAAAATCCAGATCTGCTCAACAGTGAACCCGAAAGAACTAGTGGCT 195  
QY 181 tggfaccagagaagaacagagcagccctcaactgctgatacttactggatccactagg 240  
DB 196 TGGTACACAGAGAAACA-GGCACTCTCTAACTGCTGATCTAGTGGATCCACTAGG 254  
QY 241 gaatctgggggtccctgactgcttcaagtggcagtgatctggacaagattcactctacc 300  
DB 255 GAATCTGGGCTCCCTGATCTTCACTTCAACAGAGTGAATCTGGACAGATTCACCTCACC 314  
QY 301 atcagcagcttgcagcgtgtaagaagctggcagcttattactgcagcagcattataact 360  
DB 315 ATCAGCAGTGTGACAGCTGAGACCTGGAGTTATTATTCGACAGCAATCTTAACTT 374  
QY 361 tacacgttcgacagagcagcgaagctggaataa 396  
DB 375 TTACAGTTCGGCTCGGAGCAAACTTGAAATATAA 410

RESULT 2  
LOCUS BF128999 691 bp mRNA  
DEFINITION 601811318F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4054205 5',  
mRNA sequence.  
ACCESSION BF128999  
VERSION BF128999.1 GI:10968039  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
TITLE 1 (bases 1 to 691)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

FEATURES  
source High quality sequence stop: 682.  
Location/Qualifiers  
1. 691  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4054205"  
/clone\_lib="NIH\_MGC\_48"  
/tissue="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pORF7; Site:1; XhoI;

Site-2: EcoRI: cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH-MGC Library."

BASE COUNT 160 a 175 c 178 g 176 t 2 others  
ORIGIN

Query Match 68.9%; Score 272.8; DB 144; Length 691;  
Best Local Similarity 80.6%; Pred. No. 2.3e-73;  
Matches 319; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

1 atgattcaccagccagcttcttatgtcgtcgtatggtatcgtgacccgtgag 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 170 ATGGTGTTCACAGACCCAGCTCTTCATTTCTGTTGCTCTGATCTCTGCTACGGG 229  
61 gacattgtctgacacagctccagatccctgctgtaagcttagagagagccact 120  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 230 GACATCGTATGACCCAGCTCCAGACTCCCTGGCTGTCTCTGCGCAGAGGCGCAC 289  
QY 121 attagctgaatccagctcagctgtctcaacagtagaaccgagagactactgtct 180  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 230 ATCAACTGTCAGCTCAGCAGAGCTGTTTATATACCTCCACAAATAGAACTACTAGCT 349  
QY 181 tggtaaccagaaaccagagcagcctccctaactcgtatctactgagcactag 240  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 350 TGGTACACAGCAAAACAGAGACGCTCTTAAGCTGCTCATTTACTGGCANTCTACCCG 409  
QY 241 gaattgggtccctgattcgtcctcagtgagtgatcctggagacattcactcacc 300  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 410 GAATCCGGGGTCCCTGACCGATTTCAGTGGCAGCGGCTCGGAGATTTCACTCTCAC 469.  
QY 301 atccagcgtctcagagcgtgaagcgtgagcttatctactgacacactatactt 360  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 470 ATCAGCAGCTCTCAGCTGAGATGTGCGAGTTTATTTACTGTACCAATATTATAGTACT 529  
QY 361 tacacgttcgacagggagacaaagtggaataaaa 396  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 530 GGGACGTTGGCCAGGACCAAGGTGGAATCAAA 565

RESULT 3  
LOCUS BGI48633 300 bp mRNA EST 01-FEB-2001  
DEFINITION ub5b09.v1 Soares\_mouse\_NMGB\_bcell Mus musculus cDNA clone  
IMAGE:3383368 5' similar to SW:KV4C\_HUMAN P06314 IG KAPPA CHAIN  
V-IV REGION B17 PRECURSOR. ; mRNA sequence.

ACCESSION BGI48633  
VERSION BGI48633.1 GI:12652055  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 300)  
TITLE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550

FEATURES  
SOURCE  
1.300  
/organism="Mus musculus"

/dbLxref="taxon:10090"  
/clone="IMAGE:3383368"  
/clone.lib="Soares\_mouse\_NMGB\_bcell"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: germinal B-cell; Vector: pT73D-Pac  
(pharmacia) with a modified polylinker; Site\_1: Not I;  
Site\_2: Eco RI; 1st strand cDNA was primed with a Not I -  
oligo(dT) primer [5',  
TGTACCACTGTAAGGGGAGGCGGCGCTGTTTTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.  
Library is normalized; constructed by Bento Soares and  
M.Felima Bonaldo."

BASE COUNT 85 a 72 c 79 g 64 t  
ORIGIN

Query Match 65.3%; Score 258.6; DB 174; Length 300;  
Best Local Similarity 94.9%; Pred. No. 4.4e-69;  
Matches 278; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 105 aggaagaagggccactattagctgcaaatccagtcagctgtctcaacagtagaaccg 164  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 5 AGGAGAGAGGTCACATATGAGCTGCAAAATCCAGTCAGATCTGCTCAACAGTAAACCG 64  
QY 165 agagaactactgtgtgtgtaccagcagaaccagagcagcctcctaactgtatcta 224  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 65 AAGAGACTACTGTGCTTGGTACACACAGAGGAGGAGCTCTTAACATGCTGATCTTA 124  
QY 225 ctggcattccactaggaatctggtggtccctgattcgtcagtgagtgatctggagac 284  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 125 CTGGCATTCACATAGGAGATCTGGGCTCCGTGATCGTTACAGAGCACTGATCTGGGAC 184  
QY 285 aga-cttcaactcgcacatccagcagctcgcagagcgtgaagaogtggcaattactctca 343  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 185 AGATTTTCACTCTCACATCAGCAGCTGTCAGCTGGAAGACCTGGCACTTTATTACTGCA 244  
QY 344 cgcactctataatcttaccagcttcgacagagggagacaaagtggaataaaa 396  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 245 AGCATCTTATATCTGTATACGTTTCGAGGGGGGACCAAGCTGGAATTAATAA 297

RESULT 4  
LOCUS AM405821 641 bp mRNA EST 16-FEB-2000  
DEFINITION UI-HF-B10-abp-b-07-0-UI.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
IMAGE:3057636 5' mRNA sequence.

ACCESSION AM405821  
VERSION AM405821.1 GI:6924878  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
AUTHORS 1 (bases 1 to 641)  
TITLE NIH-MGC http://mgc.ncbi.nlm.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550

FEATURES  
SOURCE  
1.641  
Location/Qualifiers

FEATURES  
SOURCE  
1.641  
Location/Qualifiers

```

/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:3057636"
/clone_lib="NH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MCC85"
/lab.host="DH10B (LTI)"
/notes="Vector: pT73-Pac; Site.1: NotI; Site.2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

```

```

BASE COUNT      159 a      178 c      163 g      141 t
ORIGIN
Query Match      64.6%; Score 256; DB 114; Length 641;
Best Local Similarity 81.0%; Pred. No. 3.5e-68;
Matches 311; Conservative 0; Mismatches 70; Indels 3; Gaps 1;

```

```

QY 16 caggttctatattgctgctgctatggtatctgacacctgtgtggagacattgtgtgaca 75
    |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 8 CAGGCTTCATTCTCTGCTGCTGATCTGCTGCTACGGGACATCGATGACCC 67
QY 76 cagttccagattccctgctgctgctgacatagagagagggccactatgtgtcaatcc 135
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||
DB 68 CAGTCTCCAGACTCCCTGCTGCTGCTGCTGCGGAGAGGGCCACCATCACTGCAAGTCC 127
QY 136 agtcaagatctgtctcaacagtagaacccagagaaactactgtgtgtacacagagaa 195
    |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 128 ACCGAGAGCTTTTATACAGCTCCACATPAGAACTACTTACTTGATGATACAGAGAA 187
QY 196 ccaaggagagctccctcaactgctgactctgtggcaatcactaggaatcgtggctcc 255
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||
DB 188 CAGGGGACCTCTCTAAGCTGCTCATTTACTGGGCACTACCCGGGAATCCGGGGTCCCT 247
QY 256 gctgctgaatgagctgagctgagctgagacattcactcctcaccagcagctgcag 315
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||
DB 248 GACCGATTGAGTGGACGGCGGCTGGGACAGATTTCACTCTCCATCCATCCAGCTGACG 307
QY 316 gctgaagacgttgacgttacttactgacgaatccta--taactttacacgttcgga 372
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||
DB 308 GCTGAGAGATGTGGCAGATTATTACTGTCAAGCAATATTATAGTACTCTCTGGAGCTTCGGC 367
QY 373 caggggaccacaagtggaataaaa 396
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||
DB 368 CAGGGGACCAAGTGGAAATCAAA 391

```

```

RESULT 5
LOCUS      AM390292      643 bp      mRNA      EST      04-FEB-2000
DEFINITION CM2-ST0182-221099-023-f04 ST0182 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AM390292
VERSION     AM390292.1 GI:6894951
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens

```

```

REFERENCE 1 (bases 1 to 643)
AUTHORS   Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     The FAPESP/LICR Human Cancer Genome Project
JOURNAL   Unpublished (1999)
COMMENT   Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
<http://www.ludwig.org.br/scripts/gethtml2.pl?rl=CM2&t2=CM2-ST0182-221099-023-f04&t3=1999-10-22&t4=1>  
 Seq primer: puc 18 forward  
 High quality sequence start: 7  
 High quality sequence stop: 641.  
 Location/Qualifiers

```

FEATURES
  source          1..643
                  /organism="Homo sapiens"
                  /db.xref="taxon:9606"
                  /clone_lib="ST0182"
                  /dev_stage="Adult"
                  /note="Organ: stomach; Vector: puc18; Site.1: SmaI;
                  Site.2: SmaI; A mini-library was made by cloning products
                  derived from ORESTES PCR (0.5. Letters Patent application
                  No. 196,716 - Ludwig Institute for Cancer Research)
                  profiles into the puc 18 vector. Reverse transcription of
                  tissue mRNA and cDNA amplification were performed under
                  low stringency conditions."
BASE COUNT      162 a      173 c      162 g      146 t
ORIGIN
Query Match      64.0%; Score 253.4; DB 114; Length 643;
Best Local Similarity 78.9%; Pred. No. 2.2e-67;
Matches 315; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

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QY 1 atgattcacagagccaggcttctatattgtctgtatggtatctgtgacacctgtgg 60
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DB 9 ATGCTGTGACAGACCCAGGCTTCATTCTCTGCTGCTGATCTGATCGCTACGGG 68
QY 61 gacattgtctgacagacagcttccagattccctgctgtaagcttagagagagggccact 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||
DB 69 GACATCGTGTAGTACCCAGTCTCCAGACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 128
QY 121 attagctgcaatccagctgacagctgctgctcaacagtagaacccagagaaactctgct 180
    ||  |||||  |||||  |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 129 ATCACTGCAAGTCCAGCCAGAGATTTTATACACTCCAAATATAGAACTTACTAGCT 188
QY 181 tggtaaccagagaagaacagggcagcctcctaactgctgacttactgtggcactaggg 240
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||
DB 189 TGGTACCAGCAGAAACAGAGACAGCTCCCTAACTCTCTCTTTACTGCGGATCTACGCGG 248
QY 241 gaatctggggtccctgatgctcagtgagtgagtgagtgagtgagtgagtgagtgagtg 300
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||
DB 249 AAATCGGGGGTCCCTGACGATTGAGTGGAGGCGGGCTGCGACAGATTCACCTCCACC 308
QY 301 atcagcagctgagcagctggaagacgttgagcttattactgtcagcagcaatccta--at 357
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||
DB 309 ATCAGCAGCTCGCAGCTGTAAGATGTGGCAGTTTATTACTGTCAAGCATTTTATTAGTCAT 368
QY 358 cttaacacgttcgagcagggaggaagtggaataaaa 396
    ||  |||||  ||  |||||  ||  |||||  ||  |||||  ||  |||||  ||  |||||  ||
DB 369 CTTCAAAAGTTCGGCCAGGACCAAGGTGGAATCAAA 407

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RESULT 6
LOCUS      BF674779      886 bp      mRNA      EST      21-DEC-2000
DEFINITION 602137932F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274551 5',
ACCESSION  BF674779
VERSION     BF674779.1 GI:11948674
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens

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REFERENCE 1 (bases 1 to 886)
AUTHORS   Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     NIH-MGC http://mgc.nci.nih.gov/
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)

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RESULT      8
LOCUS       BF663188
DEFINITION  60214432F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:429751 5',
            mRNA sequence.
ACCESSION   BF663188
VERSION     BF663188.1
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 887)
AUTHORS     NIH-MGC http://mhc.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            CDNA Library Preparation: Ling Hong/Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCML152 row: 0 column: 08
            High quality sequence stop: 691.
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            /lab_host="DH10B (phage-resistant)"
            /note="Organ: B-cells; Vector: pOT8; Site: 1: XhoI;
            Site: 2: EcoRI; CDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCACGAG(6). Size-selected >500bp
            for average insert size 1.8kb. Library constructed by Ling
            Hong in the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC library."
BASE COUNT  199 a      246 c      232 g      210 t
ORIGIN
Query Match      62.5%; Score 247.6; DB 151; Length 887;
Best Local Similarity 78.1%; Pred. No. 1.5e-65;
Matches 311; Conservative 0; Mismatches 84; Indels 3; Gaps 1;
QY 1 atgattcaacaggccaggtctctatatatgtcgtcgtatcgtgacacgtgag 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6 atggtgttgacagaccagcttctcatttctgtctgtctgagatctgtgctacgg 65
QY 61 gacatgtctgcacacagttcgaatccctggtcgttaagcttagagagagggccact 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 66 GACGTGCTGTTGACCCAGCTCCAGACTCCCTGCTGTCTCGGCGAGAGGCCAC 125
QY 121 attagctgcaatccagtcagtcgtcgtcaacagtagaaccccgaggaactacttgct 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 126 ATCAACTGCAAGTCCAGCCAGAGGTTTATACAGCTCCATATGATTAAGAACTTCTAGCT 185
QY 181 tggtaacagagaacacagagcagcctcctcaactcgtctactactcagacacagg 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 186 TGGTACACAGCTGAACAGACAGACCCCTTAACCTACTCACTTACTGGCATCAACCGG 245
QY 241 gaattcgggggtccctcgtcctcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300
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DB 246 GAATCCGGGGTCCCTCCCTTCAGTGTGAGCGAGTGGGTGGACAGATTTCACTCACTCACC 305

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QY 301 atcagcagctcgcagcgtgaagacgctgagcagttatctactcagcgaactataat--- 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 306 ATCAGCAGCTGCAGAGGTGAGATGTGGCAATTTATTTCTGTACCAATATCACTACTTCC 365
QY 358 ctctacacgltcgcagacagggagccaagctggaataaa 395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 366 CCTGGACATTCGCGCCAGAGGACCAAGGTGGAATCA 403
RESULT      9
LOCUS       AW951579
DEFINITION  EST363649 MAGE resequences, MAGB Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW951579
VERSION     AW951579.1
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 388)
AUTHORS     Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
            ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.D. and
            Quackenbush,J.
TITLE       Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
JOURNAL     Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johng@tigr.org
            Plate: 29
            Seq primer: Reverse.
FEATURES
    source
        1..388
            /organism="Homo sapiens"
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            /clone_lib="MAGE resequences, MAGB"
            /note="Vector: pBluescriptSKm"
BASE COUNT  87 a      110 c      97 g      94 t
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Query Match      61.6%; Score 244; DB 122; Length 388;
Best Local Similarity 78.6%; Pred. No. 1.5e-64;
Matches 305; Conservative 0; Mismatches 80; Indels 3; Gaps 1;
QY 10 cagggccaggtctctatatgtcgtcgtcgtatcgtgacacgtcgtgagacatgtg 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 CAGGCCAGGCTTCATTCTCTGTTCTCTGTGATCTCTGTGCTTACGGGAGACCGGTG 60
QY 70 ctgcacagctccagatccctcgtcgttaagcttagagagagggccactatagctgc 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 ATGACCAGTCTCCAGACTCCCTGCTGTCTGTGGCGCAGAGGGCACCATTAATCTGC 120
QY 130 aaatcagtcagagctcgtcgaacagtagaacccgagagaactactgtgttgtagcag 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 AGGTCCAGCAGAGATGTTTAGACAGCTCCACAACTACGAATCACTTACGCTTGATACAA 180
QY 190 cagaacacagggagcagcctcctcaactcgtatctactcgtgagcatcactaaggaatcgtgg 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 CTGAACACAGACAGCCCTCTTAACCTCTCATTTTACGTGGGCATCTACCCGGATCCGGG 240
QY 250 gtccctatcagctcagtgagcagtgagtcctgggacaattcactccacatcaagcagt 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 GTCCCTACCGATTCACTGGCAGGGGCTCTGGGACAAATTTCACTCACTCAAGGGC 300
QY 310 ctgcagcctgaagacgtgtgacgttattactcagcagcaa---tctataactccttacag 366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 CTCGAGCCTGAAGATGTGCGAGTTTATTACTGTCAAGCAATATATATTACTCGTACAAAT 360

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QY 367 ttgcagcaggagaccaggtggaataa 394  
 Db 361 TTTGGCCAGGAGCAGCTGGAATCA 388  
 RESULT 10  
 BF128829 573 bp mRNA EST 24-OCT-2000  
 LOCUS 601811013F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4053987 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF128829  
 VERSION BF128829.1 GI:10967869  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 573)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: L10M893 row: j column: 04  
 High quality sequence stop: 571.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
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 /clone\_1lb="NIH\_MGC\_48"  
 /tissue\_type="Primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;  
 Site:2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH-MGC Library."

BASE COUNT 132 a 159 c 143 g 139 t  
 ORIGIN  
 Query Match 60.8%; Score 240.6; DB 144; Length 573;  
 Best Local Similarity 78.6%; Pred. No. 1.9e-63;  
 Matches 301; Conservative 0; Mismatches 79; Indels 3; Gaps 1;  
 QY 16 caggtctatattgtctgtctatggtgacatctgtgacattgtgtgaca 75  
 Db 1 CAGGCTTCATTTCTGTCTGTCTGATCTGTGCTTACGGGACGCTGTTGACC 60  
 QY 76 cagttccagattccctggctgtgaaagctagagagagggccactatagctcaaatcc 135  
 Db 61 CAGTCTCCAGACTCCCTGGCTGTCTGTCTGCGGAGAGGGCCACCATCAATGCAAGTCC 120  
 QY 136 agtcagagctgtctcaacagtagaacccgagagagaactactgtgtgtgtacagcaaga 195  
 Db 121 AGCCAGAGAGTGTATACAGCTCAATGATTAAGAACTTCTTGTGTTGACACGCTGAAA 180  
 QY 196 ccaggagcagcctcctaaactgtgtctactgtgacatccacactgaatctgtgtccct 255  
 Db 181 CAGAGACAGCCCTCTAACTACTTATTAAGTGGCATTCACCCGGGAAATCCGGGTCCT 240

QY 256 gatcgttcagttgagcagtgatctggagacagattcactcaccatcagcagtcgag 315  
 Db 241 GCCCGCTCAGTGGCAGTGGTGTGGAGACAGATTTCATCTCACCATCAGCAGCTGGAG 300  
 QY 316 gctgaagacgtgagcagtttatactatcagcagcaatctataat---cttaacgctcga 372  
 Db 301 GCTGAAGATGTGGCAATTTATTTCTGTCCACCAATATCAATCTCCCTGGACATTCGGC 360  
 QY 373 caggagaccagagtggaataa 395  
 Db 361 CAGGAGCAGCAAGCTGGAATCA 383

RESULT 11  
 BF128587 887 bp mRNA EST 24-OCT-2000  
 LOCUS 601810838F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4054016 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF128587  
 VERSION BF128587.1 GI:10967627  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 887)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: L10M893 row: k column: 09  
 High quality sequence stop: 648.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /clone="IMAGE:4054016"  
 /clone\_1lb="NIH\_MGC\_48"  
 /tissue\_type="Primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;  
 Site:2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH-MGC Library."

BASE COUNT 228 a 261 c 228 g 170 t  
 ORIGIN  
 Query Match 58.4%; Score 231.4; DB 144; Length 887;  
 Best Local Similarity 78.6%; Pred. No. 1.5e-60;  
 Matches 290; Conservative 0; Mismatches 76; Indels 3; Gaps 1;  
 QY 31 ctgctcctataggtatctggcacctgtggtgagacattgtgtgacacagctccatccagtc 90  
 Db 8 CTGTTGCTCTGATCTCTGTCGTCGAGCGAGCATCGATGACCCAGATCTCCAGACTCC 67  
 QY 91 ctgctctgaagcttagagagagggccactatagctgcaaatcagtcagagtgctgtc 150

Db 68 CTGGCTGTGTCTCTGGCGAGAGGCCACCATCATGCAAGTCCAGCCAGAAATATTTA 127

QY 151 aacagtagaacccgagagaaactacttgcttgtagcagaagaacacggagccctc 210

Db 128 TACAACTCCAAATCATGAAACCGCTTAGCTTGACCAACAAAACCGGGACACCTCT 187

QY 211 aaactctgactactctgagatccactcactaggaatctgaggtccctgactcagtgagc 270

Db 188 AAACCTGCTATTACTGGGATCTACCCGGGAATCCGGGGTCCCTGACCATTCAGTGGC 247

QY 271 agtgcattctgagcagattcactcactcactcagcagctctgacagctgaagctgagc 330

Db 248 AGGGGCTGTGGAGACAGATTCTCACTTCACCATCAGCAGCCTGACGCTGAAGATGTGCA 307

QY 331 gttattactcagcagcaattctt---ataactctacacgtctgagcagggagcacaagt 387

Db 308 ATTATATTACGTGACGCAATTTTCAGATATTCGCCACACTTTTGCCAGGGACCAAGCTG 367

QY 388 gaaataaaa 396

Db 368 GAGATCAA 376

RESULT 12

AV685285 401 bp mRNA EST 25-SEP-2000

LOCUS AV685285 GRC Homo sapiens cDNA clone GKCFIA01 5', mRNA sequence.

DEFINITION AV685285

ACCESSION AV685285

VERSION AV685285.1 GI:10287148

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 401)

AUTHORS Wu,T., Qian,B., Peng,Y., Huang,Q., Kang,B., Gao,X., Xu,Z., Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.

TITLE Homo sapiens CDNA GK-clones

JOURNAL Unpublished (2000)

COMMENT Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn

FEATURES

source

1.401

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="GKCFIA01"

/clone\_lib="GKC"

/tissue\_type="hepatocellular carcinoma"

/dev\_stage="Adult"

/lab\_host="SOLR"

/note="Vector: pBluescript SK(+); site\_1: EcoRI; site\_2: XhoI"

BASE COUNT 78 a 112 c 109 g 102 t

ORIGIN

Query Match 58.0%; Score 229.6; DB 31; Length 401;

Best Local Similarity 76.7%; Pred. No. 4.2e-60;

Matches 296; Conservative 0; Mismatches 84; Indels 6; Gaps 1;

QY 10 cagagccaggttcttatatgctgctgctatggtatcggcaccgtggagacatgtg 69

Db 7 CAGACCCAGGCTTCATCTCTGTTGCTGTGATCTGTATCAGGGGACATCCTG 66

QY 70 ctgacacagctctcagattccctgctgctgtaagcttagagagagggccactattagctgc 129

Db 67 ATGACCAGTCTCCGCACTCCCTGCTGTGCTGTGGCGAGAGGCCACCATCAGCTGC 126

QY 130 aaatcagtagaagctctgctcactagaacccgagagaactacttgcttgtagcag 189

Db 127 AAGTCAGCCAGAGATGTTTCTACGGCCCTGGCAATTAAGATTAATCTAGCTTGCTACAG 186

QY 190 cagaacacagagcagcctcctaaactctgactcactcactcagcagcactcagcagc 249

Db 187 CAGAACCCAGACAGCCTCTCACTGCTCTCACTTACTGGGGCTGTGCTGACTCCGG 246

QY 250 gtccctgactcagctcagtgagcagtgagctcagcagcagattcactcactcagcagc 309

Db 247 GTCCCGCCGGCTTCATGTGCGAGCGGCTGTGGGACAAATTTCACTCACCACATCAGAAC 306

QY 310 ctgcagcctgaagaagctgagcagcttactcactcagcagcactt---taactctac 363

Db 307 CTACAGGCTGAGATGTGGCAGTTTATTCAGTGCAGCAATTAATACATCCTCCCTAC 366

QY 364 acgttgagcagggagcagcagctgga 389

Db 367 ACTTTGGCCAGGGGACCAAGGTGA 392

RESULT 13

AM802126 533 bp mRNA EST 16-MAY-2000

LOCUS AM802126

DEFINITION IL5-UM0071-120400-065-d06 UM0071 Homo sapiens cDNA, mRNA sequence.

ACCESSION AM802126

VERSION AM802126.1 GI:7853996

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 533)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br

FEATURES

source

1.533

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="UM0071"

/clone\_lib="UM0071"

/dev\_stage="Adult"

/note="Organ: uterus; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 131 a 145 c 137 g 120 t  
ORIGIN

Query Match 57.7% Score 228.4; DB 120; Length 533;  
Best Local Similarity 81.3%; Pred. No. 1.1e-59;  
Matches 278; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

58 gggagacatgtctgacacagatcccaatccctgctgtaagcttaagagagagggc 117  
12 CGGAGCATGCTATGATGACCCAGCTCCAGACTCCCTGCTGTCTCTGCGCAGAGGGC 71  
118 actatgctgcaaatccagctcagctgctcacaagtagaaccgagagaactctg 177  
72 ACCATCACTGCTCAAGTCCAGCCAGCTGTTTATACAGCTCCACATTAAGAACTACTTA 131  
178 gcttgtagcagcagaaccagagcagcctcctaactgctgctcactcagcagcactc 237  
132 CCTTGATACACAGAAACAGGACAGCCTCTTAAGCTCTTAATTAAGTGGCAGCTTACC 191  
238 aggaagatcggggtccctgctcagctcagctgagctgagacagagatcactc 297  
132 CGGAGATCCGGGGTCCCTGACCGATTCACTGAGCGGCTCGGAGACATTTCACTCTC 251  
238 accatcagcagctcagcagctgagacagctgagcagcttactcagcagcactc 354  
232 ACCATCAGAGCCTGAGCTGAGATGAGCAGTTTACTGTCAGCAATATTATAGT 311  
355 aactctacagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 396  
312 ACTCCCTCCTCTTCTGCGGAGGACCAAGGTGAGATCAAA 353

RESULT 14  
BF64753 558 bp mRNA EST 22-JAN-2001  
LOCUS 602267977/1 NIH\_MGC\_81 Homo sapiens cDNA clone IMAGE:4356211 5',  
DEFINITION mRNA sequence.  
ACCESSION BF64753  
VERSION BF64753.1 GI:12331968  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 558)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNU at:  
http://image.llnl.gov  
Plate: LICM1215 row: 1 column: 20  
High quality sequence stop: 558.  
Location/Qualifiers  
1..558  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4356211"  
/lab\_host="NIH\_MGC\_81"  
/note="Organ: muscle (skeletal); Vector: pDNR-LIB  
(Clontech); Site: 1; SfiI (ggcgccggccgccc); Site: 2; SfiI  
(ggcattatggcc); 5' and 3' adaptors were used in cloning  
as follows: 5' adaptor sequence: 5'-CACGCGCATTAATGACC-3'  
and 3' adaptor sequence:

FEATURES  
Source

5'-ATTCTAGAGCCGAGCGCGGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size  
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained  
inserts by PCR. This library was enriched for full-length  
clones and was constructed by Clontech Laboratories (Palo  
Alto, CA).  
BASE COUNT 129 a 152 c 146 g 131 t  
ORIGIN

Query Match 57.7% Score 228.4; DB 171; Length 558;  
Best Local Similarity 75.9%; Pred. No. 1.1e-59;  
Matches 296; Conservative 0; Mismatches 91; Indels 3; Gaps 1;

10 cagggccagatctctatattgctgctgctgagatctgagcctgagagacttg 69  
40 CAGACCCAGGCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 99  
70 ctgacacagctcctcagatccctgctgctgctgctgctgctgctgctgctgctg 129  
100 ATGACCCAGGCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 159  
130 aatccagctcagagctgctgctgctgctgctgctgctgctgctgctgctgctg 189  
160 AAGTCCAGGCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 219  
190 cagaacacagcagcagcctcctaactgctgctgctgctgctgctgctgctgctg 249  
220 CAAAAACAGGCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 279  
250 gtcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 309  
280 GTCCCGAGGCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 339  
310 ctgagcagctcagagcagctgctgctgctgctgctgctgctgctgctgctgctg 366  
340 CTGACGCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 399  
367 ttcgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 396  
400 TTGGCCAGGCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 429

RESULT 15  
BF830413 503 bp mRNA EST 13-JAN-2001  
LOCUS RCI-HR0256-021000-116-D12 HT0256 Homo sapiens cDNA, mRNA sequence.  
DEFINITION  
ACCESSION BF830413  
VERSION BF830413.1 GI:12177237  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 503)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Boridin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

TITLE  
JOURNAL  
MEDLINE  
COMMENT





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 20:39:39 ; Search time 151.39 Seconds  
(without alignments)  
1527.032 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 396

Sequence: 1 atgattaccagggccagggt.....ggaccacagtggaataaa 396

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_0401.\*  
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT.\*  
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT.\*  
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT.\*  
7: /SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT.\*  
8: /SIDS2/gcgdata/geneseq/geneseqn/NA1987.DAT.\*  
9: /SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT.\*  
10: /SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT.\*  
11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT.\*  
12: /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT.\*  
13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT.\*  
14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT.\*  
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT.\*  
16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT.\*  
17: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT.\*  
18: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	396	100.0	396	21	AS9695
2	360.8	91.1	396	21	AS9693
3	340	85.9	480	10	N91663
4	332	83.8	952	16	O94036
5	301.4	76.1	439	18	T60729
6	301.4	76.1	439	18	T60730
7	298.2	75.3	399	15	O66845
8	293.6	74.1	402	18	T43415
9	288.6	72.9	399	17	O74067
10	288.6	72.9	439	18	T60734
11	286.8	72.4	418	17	T34152

12	285.4	72.1	439	18	T72268
13	285.4	72.1	460	18	T72238
14	283.2	71.5	342	20	X34465
15	279.8	70.7	1443	15	O62958
16	279	70.5	427	20	Z32779
17	279	70.5	8068	20	Z32781
18	278.6	70.4	748	21	Z28962
19	277.8	70.2	747	19	V36237
20	275.8	69.6	870	15	O62956
21	275.2	69.5	660	14	O53430
22	270.8	68.4	330	18	V29839
23	270.6	68.3	864	20	V72072
24	270.6	68.3	2019	20	V72059
25	270.6	68.3	2025	20	V72064
26	267.2	67.5	336	20	X34588
27	267.2	67.5	1701	13	O30919
28	267.2	67.5	1701	13	O30920
29	261.4	66.0	400	9	N80499
30	260.8	65.9	511	20	V86720
31	257.4	65.0	398	15	O66699
32	257.4	65.0	798	14	O34842
33	255.2	64.4	423	20	X90025
34	253.6	64.0	463	21	O98443
35	250.2	63.2	407	13	O26047
36	248.6	62.8	402	16	T00780
37	248.6	62.8	8068	20	Z32784
38	248.2	62.7	344	13	O30900
39	247	62.4	5703	17	T34110
40	247	62.4	5703	19	V03504
41	244.8	61.8	744	20	X77243
42	241.6	61.0	336	13	O30881
43	241.6	61.0	744	20	X77247
44	241.4	61.0	339	21	A38803
45	241.2	60.9	399	21	A28641

#### ALIGNMENTS

RESULT	ID	AS9695	standard; DNA: 396 BP.
1	AS9695	standard; DNA: 396 BP.	
14-NOV-2000	(first entry)		
DNA encoding light chain variable region of humanised 3S1 antibody.			
Antibody 3D1. B7 molecule; B7: humanised immunoglobulin;			
autoimmune disease; Infectious disease; inflammatory disorder;			
systemic lupus erythematosus; diabetes mellitus; insulin; asthma;			
arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;			
multiple sclerosis; transplant rejection; proliferative disease;			
leukemia; lymphoma; anemia; sickle-cell anemia; thalassemia;			
aplastic anaemia; myeloid dysplasia syndrome; ss.			
Synthetic.			
Mus sp.			
Homo sapiens.			
Key			
CDS			
Location/Qualifiers			
1..396			
/*tag= a			
/product= "light chain variable region of 3D1 antibody"			
/note= "no termination codon given"			
1..60			
/*tag= b			
61..396			
/*tag= c			
MO200047625-A2.			

PD 17-AUG-2000.  
 XX  
 PF 09-FEB-2000; 2000MO-US03303.  
 XX  
 PR 12-FEB-1999; 99US-0249011.  
 PR 24-JUN-1999; 99US-0339596.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX  
 DR WPI; 2000-524532/47.  
 XX P-PSDB; B07966.  
 XX  
 PT Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 PS Example 3; Fig 2B; 162pp; English.  
 XX  
 CC The present sequence encodes the light chain variable region of the  
 CC humanised murine antibody 3D1. The antibody has a binding specificity to  
 CC B7 molecules. The antibody is used to construct humanized  
 CC immunoglobulins, which comprise an antigen binding region of non-human  
 CC origin and a portion of a human immunoglobulin. The humanized  
 CC immunoglobulins are useful for treating autoimmune diseases, infectious  
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinits, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 XX  
 SO Sequence 396 BP; 100 A; 96 C; 104 G; 96 T; 0 other;

Query Match 100.0%; Score 396; DB 21; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-120;  
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggaatcacaggccaggtctctatatatctgctgctatggtatctggcaccctgagg 60  
 |||||||  
 DB 1 atggaatcacaggccaggtctctatatatctgctgctatggtatctggcaccctgagg 60  
 QY 61 gacatgtgtctgacacagcttccagattccctggcgtgtaagcttagagagagggccact 120  
 |||||||  
 DB 61 gacatgtgtctgacacagcttccagattccctggcgtgtaagcttagagagagggccact 120  
 QY 121 attagctgcaaatccagctgagcttctctcaacagtagaacccgagagaaactacttgct 180  
 |||||||  
 DB 121 attagctgcaaatccagctgagcttctctcaacagtagaacccgagagaaactacttgct 180  
 QY 181 tgggtaccagagaagaacagagggcagccctctaaactgctgtaactgtagatccaccagg 240  
 |||||||  
 DB 181 tgggtaccagagaagaacagagggcagccctctaaactgctgtaactgtagatccaccagg 240  
 QY 241 gaactctgggtccctgctgctcctcagtgagctgagatctggagacagattcactctaac 300  
 |||||||  
 DB 241 gaactctgggtccctgctgctcctcagtgagctgagatctggagacagattcactctaac 300  
 QY 301 atcagagcttgcagagcttgagagacgctgttatactacgacagcaattataactctc 360  
 |||||||  
 DB 301 atcagagcttgcagagcttgagagacgctgttatactacgacagcaattataactctc 360  
 QY 361 tacacgttcgacagagggagaccaggttgaataaaa 396  
 |||||||  
 DB 361 tacacgttcgacagagggagaccaggttgaataaaa 396

RESULT 2  
 A59693  
 ID A59693 standard; DNA; 396 BP.  
 XX  
 AC A59693;  
 XX  
 DT 14-NOV-2000 (first entry)  
 XX  
 DE Nucleotide sequence of light chain variable region of 3D1 antibody.  
 XX  
 KW Antibody 3D1; B7 molecule; B7: humanised immunoglobulin;  
 KW autoimmune disease; infectious disease; inflammatory disorder;  
 KW systemic lupus erythematosus; diabetes mellitus; insulinits; asthma;  
 KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;  
 KW multiple sclerosis; transplant rejection; proliferative disease;  
 KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;  
 KW aplastic anaemia; myeloid dysplasia syndrome; ss.  
 XX  
 OS Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 XX CDS 1..396  
 FT /\*tag= a  
 FT /product= "light chain variable region of 3D1 antibody"  
 FT /note= "no termination codon given"  
 FT sig\_peptide 1..60  
 FT /\*tag= b  
 FT mat\_peptide 61..396  
 FT /\*tag= c  
 XX  
 PN W0200047625-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 09-FEB-2000; 2000MO-US03303.  
 XX  
 PR 12-FEB-1999; 99US-0249011.  
 PR 24-JUN-1999; 99US-0339596.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX  
 DR WPI; 2000-524532/47.  
 XX P-PSDB; B07964.  
 XX  
 PT Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 PS Example 1; Fig 1B; 162pp; English.  
 XX  
 CC The present sequence encodes the light chain variable region of the  
 CC murine antibody 3D1. The antibody has a binding specificity to B7  
 CC molecules. The antibody is used to construct humanized immunoglobulins,  
 CC which comprise an antigen binding region of non-human origin and a  
 CC portion of a human immunoglobulin. The humanized immunoglobulins are  
 CC useful for treating autoimmune diseases, infectious diseases,  
 CC inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinits, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 XX  
 SO Sequence 396 BP; 98 A; 97 C; 104 G; 97 T; 0 other;

Query Match 91.1%; Score 360.8; DB 21; Length 396;



Best Local Similarity 94.4%; Pred. No. 3.1e-108;  
Matches 374; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 atgattacacagccaggtcttattatgtctgtatggtatctgcaactgtgg 60  
1 atgattacacagccaggtcttattatgtctgtatggtatctgcaactgtgg 60  
Db 1 atgattacacagccaggtcttattatgtctgtatggtatctgcaactgtgg 60  
QY 61 gaattgtgtgacagcttccagatccctgtgcttaagcttagagagagggcact 120  
61 gaattgtgtgacagcttccagatccctgtgcttaagcttagagagagggcact 120  
Db 61 gaattgtgtgacagcttccagatccctgtgcttaagcttagagagagggcact 120  
QY 121 atgacgtcgaatccagctcagatctgtcacaagtagaacccagagaaactgtgct 180  
121 atgacgtcgaatccagctcagatctgtcacaagtagaacccagagaaactgtgct 180  
Db 121 atgacgtcgaatccagctcagatctgtcacaagtagaacccagagaaactgtgct 180  
QY 181 tggtaaccagagaacacagagggcagctcctaactgtgatactgtggcaactagg 240  
181 tggtaaccagagaacacagagggcagctcctaactgtgatactgtggcaactagg 240  
Db 181 tggtaaccagagaacacagagggcagctcctaactgtgatactgtggcaactagg 240  
QY 241 gaattgtgtgctcctgtatcgtcagtgagtgatctggagagatttcaactcacc 300  
241 gaattgtgtgctcctgtatcgtcagtgagtgatctggagagatttcaactcacc 300  
Db 241 gaattgtgtgctcctgtatcgtcagtgagtgatctggagagatttcaactcacc 300  
QY 301 atcagcagctcgcagctgaaagacgttgcaatttacttcaacgcaacttataatcct 360  
301 atcagcagctcgcagctgaaagacgttgcaatttacttcaacgcaacttataatcct 360  
Db 301 atcagcagctcgcagctgaaagacgttgcaatttacttcaacgcaacttataatcct 360  
QY 361 tacacgttcgcagacaggggacccaaggttgaaataaa 396  
361 tacacgttcgcagacaggggacccaaggttgaaataaa 396  
Db 361 tacacgttcgcagacaggggacccaaggttgaaataaa 396

RESULT 3

ID N91663 standard; DNA; 480 BP.  
XX N91663;  
AC  
XX  
DT 14-MAR-1990 (first entry)  
XX  
DE Light chain of monoclonal antibody 6A4.  
XX  
KM Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.  
XX  
FH Key Location/Qualifiers  
FT CDS 37..480  
FT /\*tag= a  
XX  
PN EP338395-A.  
PD 25-OCT-1989.  
XX  
PF 12-APR-1989; 89EP-0106463.  
XX  
PR 19-APR-1988; 88DE-3813023.  
XX  
PA (BEHW ) BEHRINGWERKE.  
XX  
PI Domdey H, Marget M, von Specht BU;  
XX  
DR WPI: 1989-310861/43.  
DR P-PSDB; P93078.  
XX  
PT Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for  
XX  
PS variable antibody regions.  
XX  
PS Claim 1; page 6; 7pp; german.  
XX  
CC The sequence has a variable and constant region. Monoclonal antibody 6A4  
CC reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa.  
CC It is used for therapy and diagnosis of infection, and as a carrier for  
CC drugs. The antibody is IgG2a subclass.  
XX

SO Sequence 480 BP; 115 A; 118 C; 135 G; 112 T; 0 other;

Query Match 85.9%; Score 340; DB 10; Length 480;  
Best Local Similarity 91.2%; Pred. No. 2.1e-101;  
Matches 361; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 atgattacacagccaggtcttattatgtctgtatggtatctgcaactgtgg 60  
1 atgattacacagccaggtcttattatgtctgtatggtatctgcaactgtgg 60  
Db 37 atgattacacagccaggtcttattatgtctgtatggtatctgcaactgtgg 96  
QY 61 gaattgtgtgacagcttccagatccctgtgcttaagcttagagagagggcact 120  
61 gaattgtgtgacagcttccagatccctgtgcttaagcttagagagagggcact 120  
Db 97 gaattgtgtgacagcttccagatccctgtgcttaagcttagagagagggcact 156  
QY 121 atgacgtcgaatccagctcagatctgtcacaagtagaacccagagaaactgtgct 180  
121 atgacgtcgaatccagctcagatctgtcacaagtagaacccagagaaactgtgct 180  
Db 157 atgacgtcgaatccagctcagatctgtcacaagtagaacccagagaaactgtgct 216  
QY 181 tggtaaccagagaacacagagggcagctcctaactgtgatactgtggcaactagg 240  
181 tggtaaccagagaacacagagggcagctcctaactgtgatactgtggcaactagg 240  
Db 217 tggtaaccagagaacacagagggcagctcctaactgtgatactgtggcaactagg 276  
QY 241 gaattgtgtgctcctgtatcgtcagtgagtgatctggagagatttcaactcacc 300  
241 gaattgtgtgctcctgtatcgtcagtgagtgatctggagagatttcaactcacc 300  
Db 277 gaattgtgtgctcctgtatcgtcagtgagtgatctggagagatttcaactcacc 336  
QY 301 atcagcagctcgcagctgaaagacgttgcaatttacttcaacgcaacttataatcct 360  
301 atcagcagctcgcagctgaaagacgttgcaatttacttcaacgcaacttataatcct 360  
Db 337 atcagcagctcgcagctgaaagacgttgcaatttacttcaacgcaacttataatcct 396  
QY 361 tacacgttcgcagacaggggacccaaggttgaaataaa 396  
361 tacacgttcgcagacaggggacccaaggttgaaataaa 396  
Db 397 cgacgttcggtgagagacccaagcttgaaataaa 432

RESULT 4

ID O94036 standard; CDNA; 952 BP.  
XX O94036;  
AC  
XX  
DT 21-NOV-1995 (first entry)  
XX  
DE Mab 55.1 light chain CDNA.  
XX  
KM Antigen binding structure; complementarity determining region; CDR,  
KM CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
KM monoclonal antibody; Mab; immunotherapy; therapy; diagnosis;  
KM transgenic animal; transgenic plant; antibody engineering;  
KM humanized antibody; immunotoxin; ss.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 16..735  
FT /\*tag= a  
FT sig\_peptide 16..75  
FT /\*tag= b  
FT mat\_peptide 76..732  
FT /\*tag= c  
XX  
PN W09515382-A.  
PD 08-JUN-1995.  
XX  
PF 29-NOV-1994; 94MO-GB02610.  
XX  
PR 03-JUN-1994; 94GB-0011089.  
PR 03-DEC-1993; 93GB-0024819.  
XX  
PA (ZENEC ) ZENECAL LTD.  
XX

PI Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS.  
 PI Rose MS, Wright AF;  
 DR WPI: 1995-215262/28.  
 DR P-PSDB: R76087.  
 XX  
 XX Antigen binding structures containing CDRs recognising the CA55.1  
 PT antigen - produced by hybridomas and host cells, for use in the  
 PT diagnosis and therapy of cancer  
 XX  
 PS Disclosure: Fig.16; 121pp; English.  
 XX  
 XX MAB 55.1 (BCACC 93081901) recognises the colorectal tumor-associated  
 CC antigen CA55.1. CDNA's for the heavy (Q94037) and light (Q94036)  
 CC chains of 55.1 were isolated, and F(ab)'<sub>2</sub>, Fab, Fv, scFv or  
 CC V-min humanized 55.1 constructs have been expressed in myeloma  
 CC cells and E. coli.  
 CC  
 XX  
 XX Sequence 952 BP; 245 A; 268 C; 215 G; 224 T; 0 other;

Query Match 83.8%; Score 332; DB 16; Length 952;  
 Best Local Similarity 89.9%; Pred. No. 1.1e-98;  
 Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 1 atgagttcacagccaggttcttatatgtcgtcgtcgtatggtatcgtgacactgtgag 60  
 DB 16 atgagttcacagccaggttcttatatgtcgtcgtcgtatggtatcgtgacactgtgag 75  
 OY 61 gacatgtgtcgtcacacagtcctccagaatccctggtcgtgttaagcttagagagagccact 120  
 DB 76 gacatgtgtcgtcacacagtcctccagaatccctggtcgtgttaagcttagagagagccact 135  
 OY 121 attagctgaatccagtcagtcagtcgtcctcaacagtcagtcagtcagtcagtcagtcagtc 180  
 DB 136 atgagtcgaatccagtcagtcagtcgtcctcaacagtcagtcagtcagtcagtcagtcagtc 195  
 OY 181 tggtaacagcagaagagcagtcctcctaaactgtatctactcgtggtcagtcagtcagtcagtc 240  
 DB 196 tggtaacagcagaagagcagtcctcctaaactgtatctactcgtggtcagtcagtcagtcagtc 255  
 OY 241 gaatctgggtggtccctgagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300  
 DB 256 aacatctgggtggtccctgagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 315  
 OY 301 atcagcagtcgtcagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 360  
 DB 316 atcagcagtcgtcagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 375  
 OY 361 tacacgtctcagcagcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 396  
 DB 376 cygagctcgtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 411

RESULT 5  
 T60729  
 ID T60729 standard; CDNA: 439 BP.  
 XX  
 AC T60729:  
 XX  
 DT 25-SEP-1997 (first entry)  
 DE  
 XX  
 XX CDNA encoding humanised murine anti-E-selectin antibody CY1788V(LA).  
 KM Humanised: murine; mouse; E-selectin; antibody; light chain;  
 KM variable region; detection; inhibition; mediation; cell adhesion;  
 KM diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;  
 KM acute respiratory distress syndrome; gross cystic breast disease;  
 KM cancer; treatment; splanchmic occlusion shock; psoriasis;  
 KM complement; chimeric; ds.  
 XX  
 OS Chimeric - Mus spp.  
 OS Chimeric - Homo sapiens.

OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 16..426  
 FT /tag= a  
 FT /note= "no stop codon given"

XX W09640942-A1.  
 XX  
 XX 19-DEC-1996.  
 XX  
 XX 06-JUN-1996; 96WO-0509204.  
 XX  
 XX 07-JUN-1995; 95US-0482112.  
 XX  
 XX (CYTE-) CYTEL CORP.  
 XX  
 XX Bending MM, Jones ST, Perez C, Saldanha JW, Williams MA;  
 PI Jones S;  
 XX  
 DR WPI: 1997-077272/07.  
 DR P-PSDB: W10544.  
 XX  
 XX Humanised anti-E-selectin antibody - useful for diagnosis and  
 PT treatment of, e.g. inflammatory responses, septic shock, acute  
 PT respiratory distress syndrome or cancer  
 XX  
 PS Claim 29; Page 69; 89pp; English.

XX The present sequence encodes the humanised murine anti-E-selectin  
 CC antibody (Ab) light chain variable region, CY1788V(LA). The Ab can  
 CC be used to detect E-selectin, or inhibit E-selectin mediated cell  
 CC adhesion. It can also be used to diagnose, reduce or inhibit an  
 CC inflammatory response, or the severity of pathologies, e.g. septic  
 CC shock, acute respiratory distress syndrome, wound associated  
 CC sepsis, gross cystic breast disease or cancer, or treat, e.g.  
 CC splanchmic occlusion shock, or psoriasis. It can be administered to  
 CC a human without inducing an immune response. In addition, the  
 CC effector portion of the Ab can interact with various components of  
 CC the human immune system, including complement.

SQ Sequence 439 BP; 106 A; 110 C; 117 G; 106 T; 0 other;

Query Match 76.1%; Score 301.4; DB 18; Length 439;  
 Best Local Similarity 86.5%; Pred. No. 8.1e-89;  
 Matches 345; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

OY 1 atgagttcacagccaggttcttatatgtcgtcgtcgtatggtatcgtgacactgtgag 60  
 DB 28 atgagttcacaggttcttatatgtcgtcgtcgtatggtatcgtgacactgtgag 87  
 OY 61 gaatctgggtggtccctgagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 120  
 DB 88 gaatctgggtggtccctgagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 147  
 OY 121 attagctgaatccagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 180  
 DB 148 atcaactgcaagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 207  
 OY 181 tggtaacagcagaagagcagtcctcctaaactgtatctactcgtggtcagtcagtcagtcagtc 240  
 DB 208 tggtaacagcagaagagcagtcctcctaaactgtatctactcgtggtcagtcagtcagtcagtc 267  
 OY 241 gaatctgggtggtccctgagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300  
 DB 268 gaatctgggtggtccctgagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 327  
 OY 301 atcagcagtcgtcagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 357  
 DB 328 atcagcagtcgtcagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 387  
 OY 358 cttaacagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 396



/note="complementarity determining region 1 of

\_\_\_\_\_



DE	XX	CDNA encoding wild type murine anti-E-selectin antibody CY1787V(L).
XX	XX	
XX	XX	Humanised; murine; mouse; E-selectin; antibody; light chain;
XX	XX	variable region; detection; inhibition; mediation; cell adhesion;
XX	XX	diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
XX	XX	acute respiratory distress syndrome; gross cystic breast disease;
XX	XX	cancer; treatment; splanchic occlusion shock; psoriasis;
XX	XX	complement; ds.
XX	XX	
OS	XX	Mus spp.
XX	XX	
EH	XX	Location/Qualifiers
FT	XX	16..426
FT	XX	/*tag= a
FT	XX	/note= "no stop codon given"
XX	XX	
PN	XX	MO9640942-AL.
XX	XX	
PD	XX	19-DEC-1996.
XX	XX	
PF	XX	06-JUN-1996; 96WO-US09204.
XX	XX	
PR	XX	07-JUN-1995; 95US-0482112.
XX	XX	
PA	XX	(CYTE-) CYTEL CORP.
XX	XX	
PI	XX	Bendig MM, Jones ST, Perez C, Salama JW, Williams MA;
PI	XX	Jones S;
DR	XX	WPI: 1997-077272/07.
XX	XX	P-PSDB: W10547.
XX	XX	
PT	XX	Humanised anti-E-selectin antibody - useful for diagnosis and
PT	XX	treatment of, e.g. inflammatory responses, septic shock, acute
PT	XX	respiratory distress syndrome or cancer
XX	XX	
PS	XX	Example II; Page 55; 89pp; English.
XX	XX	
CC	XX	The present sequence encodes the wild type murine anti-E-selectin
CC	XX	antibody (Ab) light chain variable region, CY1787V(L), which was
CC	XX	used in the preparation of the humanised anti-E-selectin Ab
CC	XX	chain variable regions, CY1788V(LA-B). The humanised Ab can
CC	XX	be used to detect E-selectin, or inhibit E-selectin mediated cell
CC	XX	adhesion. They can also be used to diagnose, reduce or inhibit an
CC	XX	inflammatory response, or the severity of pathologies, e.g. septic
CC	XX	shock, acute respiratory distress syndrome, wound associated
CC	XX	sepsis, gross cystic breast disease or cancer, or treat, e.g.
CC	XX	splanchnic occlusion shock, or psoriasis. They can be administered
CC	XX	to a human without inducing an immune response. In addition, the
CC	XX	effector portion of the Ab can interact with various components of
CC	XX	the human immune system, including complement.
XX	XX	
XX	XX	Sequence 439 BP; 108 A; 110 C; 116 G; 105 T; 0 other;

Query Match	72.9%	Score 288.6	DB 18	Length 439
Best Local Similarity	84.5%	Pred. No. 1.2e-84		
Matches 537	Conservative 0	Mismatches 59	Indels 3	Gaps 14
Qy	1	atgagatccagagcccaagttctctatattgctgcgcgtcgtatgggtatctcgcacctgtgg	60	
	28	atggagtcacagaccagctcaggtctctatgttcctgcgtcgtgtctgtgtatctgttaccctgtgg	87	
Db	61	gacattctgctctgcaacagatctccagattccctctgctgtctgaagcttagggagagagggacc	120	
	88	gacattctgctctgcaacagatctccagattccctctgctgtctgaagcttagggagagagggacc	147	
Qy	121	atgaagcgaatcccaagtcagagctctgtcccaacagtagaaccggagagaactactgtgt	180	
	148	atgagctgcgaatcccaagtcagagctctgtcccaacagtagaaccggagagaactactgtgt	207	
Db	181	tggtaccagcagaaaccagagggcagctctcttaaacctgctatctatctatctgcatccactagg	240	

Accession	Sequence	Position
D8	tggtaccgcgcagaaacccgagcgacgcttccaaacctgtgtactatcctggcattccaccagg	267
Q7	gaatctgggtgtccctcgatcgcgtctcaagtgcagctgagatctgtgggaacagattccactcac	300
D8	gaatctgggtgtccctcgatcgcgtctcaacgagcagctgagatctgtgggaacagattccactcac	327
Q7	atcagcagctctgcagagctcgtgaagacgttgcgaatttattactacacgcatctata---at	357
D8	atcagcagctctgcagagctcgtgaagacgttgcgaatttattactacgcatctataatagttat	387
Q7	cttaccagcttcgcgcaggggacacaaagttgnaataa	396
D8	ccgctcacgcttcgtcgtcgtggacaagcttgagcttgaa	426

RESULT	11	
XX	T34152	T34152 standard; DNA: 418 BP.
XX	T34152	
XX	T34152;	
XX	14-FEB-1997	(first entry)
XX	Monoclonal antibody PA1-3F10	variable light chain-encoding DNA.
XX	PA1-3F10; antibody;	hybridoma; LMBP1322CB; cancer; target; epitope;
XX	killing; colorectal;	lung; ovary; cytotoxin; neoplasia; ss.
XX	Mus musculus.	
XX	Key	Location/Qualifiers
XX	FT CDS	2..418
XX	FT	/*tag= a
XX	FT	/note= "no start or stop codon"
XX	PN	W09622310-A1.
XX	PD	25-JUL-1996.
XX	PF	15-JAN-1996; 96MO-SE00029.
XX	PR	18-JAN-1995; 95SE-0000148. }
XX	PA	(BIOT-) BIOINVENT INT AB.
XX	PI	Carlsson R, Jansson B;
XX	DR	WPI: 1996-354478/35.
XX	DR	P-PSDB; R99469.
XX	PT	Monoclonal antibody PA1-3F10 produced by hybridoma BCCM LMBP1322CB -
XX	PS	useful to target cancer cells for killing or detection
XX	XX	Claim 10; Fig 10; 62pp; English.
XX	T34152	encodes the variable light (VL) chain of monoclonal antibody
XX	PA1-3F10	produced by hybridoma BCCM LMBP1322CB. The antibody is
XX	CC	directed against an epitope present on cancer cells, in particular
XX	CC	breast, ovary, lung and colorectal cancer cells. The antibody is
XX	CC	useful for detecting cancer cell epitopes and hence in the diagnosis
XX	CC	of cancer. The antibody can be conjugated to a cytotoxic compound and
XX	CC	targeted to cancer cells to kill them.
XX	Sequence	418 BP; 102 A; 100 C; 107 G; 109 T; 0 other;
XX	Query Match	72.4%; Score 286.8; DB 17; Length 418;
XX	Best Local Similarity	84.8%; Pred. No. 4.7e-84;
XX	Matches 334; Conservative	0; Mismatches 57; Indels 3; Gaps 1;
XX	6	ttcaagagcccaagctctatatgtcgtcgctatggtatctgacacctgaggacat 65



PF 25-OCT-1996; 96EP-0117154.  
 XX  
 PR 06-NOV-1995; 95EP-0117407.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 PI Bendig M, Jones T, Saldana J;  
 XX WPI: 1997-334904/31.  
 DR P-PSDB: W21653.  
 XX  
 PT Humanised form of murine monoclonal antibody Mab 15 - useful for  
 XX treating lung cancer  
 PS  
 XX Claim 14: Fig 1: 71pp: English.  
 CC This cDNA sequence encodes the light chain variable region VL  
 CC (W21653) of murine monoclonal antibody (Mab) 15 (DSM ACC2117),  
 CC a Mab that shows a therapeutic effect on human tumour cells,  
 CC especially human lung cancer. The clone was isolated from  
 CC hybridoma cDNA using a degenerate leader sequence primer (T72239)  
 CC and a kappa constant region reverse primer (T72240). The VH region  
 CC (see T72267) was also amplified. The VL and VH sequences were  
 CC used in a claimed process for the production of novel humanised,  
 CC reshaped Mab 15 having humanised, reshaped VL and VH sequences  
 CC (see W21651 and W21652), which can be used for treating tumours,  
 CC especially lung cancer, and for the manufacture of a drug related  
 CC to tumours, especially lung cancer.  
 XX  
 SO Sequence 460 BP; 112 A; 118 C; 113 G; 117 T; 0 other;

Query Match 72.1%; Score 285.4; DB 18; Length 460;  
 Best Local Similarity 84.0%; Pred. No. 1.4e-83;  
 Matches 335; Conservative 0; Mismatches 61; Indels 3; Gaps 1;  
 QY 1 atgagatcacagagccaggttcttatatgctgctgctatggatctgacccctgtgg 60  
 DB 13 atgagatcacatccctggtcttcttatgctgctgctatggatctgacccctgtgg 72  
 QY 61 gacatgctgctgacagctccagatctccctgctgctgctgctgctgctgctgctgct 120  
 DB 73 gacatgctgctgacagctccagatctccctgctgctgctgctgctgctgctgctgct 132  
 QY 121 atgagctgaagaatccagctcagctcagctcagctcagctcagctcagctcagctcagct 180  
 DB 133 atgagctgcaagctcagctcagctcagctcagctcagctcagctcagctcagctcagct 192  
 QY 181 tggctacagcagaacacagcagcagctcctctaaactgctgctgctgctgctgctgctgct 240  
 DB 193 tggctacagcagaacacagcagcagctcctctaaactgctgctgctgctgctgctgctgct 252  
 QY 241 gaatcctggggtccctgctcagctcagctcagctcagctcagctcagctcagctcagctcagct 300  
 DB 253 gaatcctggggtccctgctcagctcagctcagctcagctcagctcagctcagctcagctcagct 312  
 QY 301 atcagcagctcagcagctcagcagctcagcagctcagcagctcagcagctcagcagctcagcagct 357  
 DB 313 atcagcagctcagcagctcagcagctcagcagctcagcagctcagcagctcagcagctcagcagct 372  
 QY 358 ccttaccagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 396  
 DB 373 ccttaccagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 411

RESULT 14  
 X34465  
 ID X34465 standard; cDNA: 342 BP.  
 XX  
 AC X34465;  
 XX  
 DT 25-JUN-1999 (first entry)  
 XX

DE Mouse Mab 6A4 light chain variable region encoding DNA.  
 XX  
 KW Rolling template; nucleic acid synthesis; polynucleotide polymerase;  
 KW gene production; primer; monoclonal antibody; 6A4; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN W09914370-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 15-SEP-1998; 98WO-US19157.  
 XX  
 PR 15-SEP-1997; 97US-0929856.  
 XX  
 PA (HIAT/) HIATT A C.  
 PA (ROSE/) ROSE F D.  
 XX  
 PI Hiatt AC, Rose FD;  
 XX  
 DR WPI: 1999-244045/20.  
 DR P-PSDB: Y06830.  
 XX  
 PT Producing specific polynucleotides using rolling templates  
 XX  
 PS Example 6; Page 40; 109pp: English.  
 XX

The invention relates to a method for producing polynucleotides having a defined sequence using rolling templates that successively add nucleotides (nts) to a longer primer strand. The method comprises: (1) incubating, under annealing conditions, a primer and a template that has a 5'-region not complementary to the primer, a 3'-region complementary to the 3'-end of primer and a non-reactive 3'-terminus, with the template being shorter than the primer; (ii) reacting the primer with at least one nt in presence of a template-dependent polynucleotide polymerase to extend it by at least one nt (complementary to the 5'-region of template) at its 3'-end; (iii) separating the template and the extended primer; and (iv) repeating the cycle of (i)-(iii) as often as needed to synthesize the desired polynucleotide. The method is especially used to produce genes or their segments. The method provides fast, accurate, inexpensive synthesis of RNA or DNA and is more efficient than chemical coupling processes. It has higher specificity and eliminates the need for protection. The products can be cloned directly. The method avoids problems of waste disposal and includes an inherent editing effect (failure sequences will not be extended further in subsequent rounds) so that purification of the end product is facilitated. Synthesis may take place on a vector, simplifying cloning and sequences with codon usage optimized for a particular host can be prepared. This represents the nucleotide sequence of the light chain variable region of the mouse monoclonal antibody (Mab) 6A4, synthesised by the method of the invention.

Query Match 71.5%; Score 283.2; DB 20; Length 342;  
 Best Local Similarity 90.2%; Pred. No. 6.4e-83;  
 Matches 303; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
 QY 61 gacatgctgctgacacagctcctcagatctccctgctgctgctgctgctgctgctgctgct 120  
 DB 1 gacatgctgctgacacagctcctcagatctccctgctgctgctgctgctgctgctgctgct 60  
 QY 121 atgagctgaagaatccagctcagctcagctcagctcagctcagctcagctcagctcagctcagct 180  
 DB 61 atgagctgaagaatccagctcagctcagctcagctcagctcagctcagctcagctcagctcagct 120  
 QY 181 tggctacagcagaacacagcagcagctcctctaaactgctgctgctgctgctgctgctgctgct 240  
 DB 121 tggctacagcagaacacagcagcagctcctctaaactgctgctgctgctgctgctgctgctgct 180  
 QY 241 gaatcctggggtccctgctcagctcagctcagctcagctcagctcagctcagctcagctcagct 300



Db, 181 gaatctggggtccctgacgtcttcacagcagtgatctggtgacagattcactcacc 240  
QY 301 atcagcagctgtagcagctgaagacgctgtagcttattacgcagcaatcttaattc 360  
Db 241 atcagcagctgtagcagctgaagacgctgtagcttattacgcagcaatcttaattc 300  
QY 361 tacacgttcgacaggggacccaaggtggaataaaa 396  
Db 301 cggacgtctgctgtagcagccaagctggaataaaa 336  
RESULT 15  
Q62958  
ID Q62958 standard; DNA; 1443 BP.  
XX Q62958;  
AC Q62958;  
DT 09-SEP-1994 (first entry)  
XX Glycophorin antibody IC3 Fab coding region.  
DE Glycophorin antibody IC3 Fab coding region.  
XX Glycophorin; antibody IC3; target binding polypeptide; PCR;  
KM polymerase chain reaction; primer; antibody engineering;  
KW humanized antibody; phagemid pHFA; plasmid p569;ss.  
XX  
OS Synthetic.  
XX  
PN WO9407921-A.  
XX  
PD 14-APR-1994.  
XX  
PF 24-SEP-1993; 93WO-AU00491.  
XX  
PR 25-SEP-1992; 92AU-0004973.  
XX  
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX  
PI Atwell JL, Colman PM, Hudson PJ, Irving RA, Kortt A;  
PI Lah M, Malbyrl, Power BE;  
XX  
XX WPI; 1994-135515/16.  
XX  
XX  
XX New target-binding polypeptide(s) used for diagnosis, etc. -  
XX having a stable core polypeptide region with at least one  
XX target-binding region covalently attached, opt. mutated to alter  
XX specificity, etc.  
XX  
XX Disclosure; Page 42; 67pp; English.  
XX  
XX PCR primers given in 062951-52 were used to clone anti-glycophorin  
XX antibody IC3 Fab coding region. The DNA sequence of the first 1443  
XX bases of the Fab fragment in pHFA, ready for ligation post PCR  
XX amplification for ligation into p569, is given in 062958.  
XX  
SQ Sequence 1443 BP: 391 A; 388 C; 351 G; 313 T; 0 other;  
Query Match 70.7%; Score 279.8; DB 15; Length 1443;  
Best Local Similarity 84.6%; Pred. No. 1.5e-81;  
Matches 314; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 206 ctctaaactgctgacttactggtgacatccactaggggaatctgggtccctgacgttca 265  
Db 914 ctctaaaccgctgacttactggtgacatccactaggggaatctgggtccctgacgttca 973  
QY 266 gtagcagtgatctgtagcagagatttcactctcaccatcagcagctgcaagctgaagacg 325  
Db 974 cagcagtgatctgtagcagagatttcactctcaccatcagcagctgcaagctgaagacg 1033  
QY 326 tggcagtttactctgacgcaatctataatcttcaacgttcgacaggggacccaag 385  
Db 1034 tggcagtttactctgacgcaatctataatcttcaacgttcgacaggttgcgtggaaccaagc 1093  
QY 386 tggaaataaaa 396  
Db 1094 tggaaataaaa 1104

Search completed: April 29, 2001, 20:39:41  
Job time: 3488 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 25, 2001, 09:39:40 ; Search time 24.35 Seconds  
(without alignments)  
372.543 Million cell updates/sec

Title: US-09-249-011-8

Perfect score: 681

Sequence: 1 MDSQAQVILILLWVSGTGC.....YCTQSYNLYTFGQGTKEIK 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_67:\*

1: pir1:\*\n2: pir2:\*\n3: pir3:\*\n4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	596	87.5	133	2 PS0023	Ig kappa chain pre
2	558.5	82.0	134	1 K4HUI7	Ig kappa chain pre
3	558	81.9	120	2 G33932	Ig kappa chain pre
4	553.5	81.3	134	2 S49531	anti-Sm antibody V
5	552	81.1	133	1 K4HUI7	Ig kappa chain pre
6	542.5	79.7	138	2 S26040	Ig kappa chain pre
7	541.5	79.5	145	2 PL0014	Ig kappa chain pre
8	539.5	79.2	134	2 PC1214	Ig kappa chain pre
9	536.5	78.8	135	2 S38807	Ig kappa chain pre
10	536	78.7	135	2 A53261	Ig kappa chain pre
11	535.5	78.6	129	2 S40347	Ig kappa chain - h
12	532.5	78.2	240	2 S06084	Ig kappa chain pre
13	528.5	77.6	132	2 S46373	Ig kappa chain pre
14	515.5	75.7	134	2 S21917	Ig kappa chain V-J
15	515	75.6	121	1 K4HU	Ig kappa chain V r
16	510	74.9	113	2 PT0407	Ig kappa chain pre
17	506.5	74.4	120	2 S51147	Ig light chain V r
18	506.5	74.4	124	2 S40364	antibody light cha
19	506	74.3	112	2 S43103	Ig kappa chain - h
20	502.5	73.8	113	2 S34002	Ig kappa chain V-J
21	500.5	73.5	136	2 A49137	Ig kappa chain V r
22	497.5	73.1	114	1 K4HUI7	Ig kappa chain pre
23	494	72.5	112	2 PL0265	Ig kappa chain V-I
24	493.5	72.5	129	2 S40329	Ig kappa chain V-J
25	492	72.2	113	2 PT0408	Ig kappa chain V r
26	490.5	72.0	113	2 S30520	Ig light chain V r
27	482	70.8	112	2 S41393	Ig kappa chain V r
28	480	70.5	103	2 PH1047	Ig kappa chain V r
29	476.5	70.0	113	2 S34003	Ig light chain V r

30	475	69.8	103	2 PH1052	Ig light chain V r
31	473.5	69.5	111	2 S03304	Ig kappa chain V r
32	473.5	69.5	114	2 S44116	Ig kappa chain V-J
33	473.5	69.5	114	2 S44119	Ig kappa chain V-J
34	471	69.2	104	2 PH1101	Ig light chain V r
35	470.5	69.1	113	2 S30523	Ig kappa chain V r
36	470	69.0	104	2 PH1102	Ig light chain V r
37	467	68.6	103	2 PH1051	Ig light chain V r
38	466	68.4	104	2 PH1104	Ig light chain V r
39	464	68.1	103	2 PH1050	Ig light chain V r
40	462.5	67.9	113	2 PL0263	Ig kappa chain V r
41	460	67.5	101	2 PH1046	Ig light chain V r
42	457	67.1	104	2 PH1103	Ig light chain V r
43	452.5	66.4	113	2 PL0264	Ig kappa chain V r
44	452.5	66.4	214	2 S68212	Ig kappa chain V r
45	452	66.4	106	2 A49138	Ig kappa chain V r

## ALIGNMENTS

RESULT 1  
PS0023  
Ig kappa chain precursor V region (6A4) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000  
C:Accession: PS0023  
R:Margel, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Dondey, H.  
Gene 74, 335-345, 1988  
A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains  
A:Reference number: PS0023; M01D:89232725  
A:Accession: PS0023  
A:Molecule type: mRNA  
A:Residues: 1-133 <MAR>  
A:Experimental source: strain BALB/c  
A:Note: the amino-terminal four residues of the mature protein were directly sequence  
C:Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aer  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-133/Product: Ig kappa chain V region 6A4 #status experimental <IGV>  
F:36-116/Domain: immunoglobulin homology <IMV>

Query Match 87.5%; Score 596; DB 2; Length 133;  
Best Local Similarity 86.4%; Pred. No. 8.6e-44;  
Matches 114; Conservative 10; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MDSQAQVILILLWVSGTGDIVLTQSPDSLAVSLGRATISCKSSQSLNSRTRENYLA 60  
|||||  
Db 1 MDSQAQVILILLWVSGTGDIVWSSPSSLAWSAGKVTMSCKSSQSLNSTKRFELA 60  
QY 61 WYQKPGQPKLLIYMASTRSGVDPDRFGSGSTDTLTSSLAQADVAVYCTQSYNL 120  
|||||  
Db 61 WYQKPGQPKLLIYMASTRSGVDPDRFGSGSTDTLTSSLAQADVAVYCTQSYNL 120  
QY 121 YTFGQGTKEIK 132  
|||  
Db 121 RTFGGQGTKEIK 132  
RESULT 2  
K4HUI7  
Ig kappa chain precursor V-IV region (B17) - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 21-Jan-2000  
C:Accession: A01905  
R:Marsh, P.; Mills, F.; Gould, H.  
Nucleic Acids Res. 13, 6531-6544, 1985  
A:Title: Detection of a unique human VkapapIV germline gene by a cloned cDNA probe.  
A:Reference number: A01905; M01D:86041854  
A:Accession: A01905  
A:Molecule type: mRNA

A:Residues: 1-134 <MAR>  
A:Note: the sequence was determined from the differentiated gene  
A:Note: the authors translated the codon TGC for residue 76 as Trp  
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into higher order structures.  
C:Superfamily: immunoglobulin v region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
E:1-20/Dominant: signal sequence #status predicted <SIG>  
E:21-134/Product: Ig kappa chain v-IV region (B17) #status predicted <MAT>  
F:21-43/Region: framework 1  
F:36-116/Dominant: immunoglobulin homology <IMW>  
F:44-60/Region: complementarity-determining 1  
F:61-75/Region: framework 2  
F:76-82/Region: complementarity-determining 2  
F:83-114/Region: framework 3  
F:115-121/Region: complementarity-determining 3  
F:122-134/Region: framework 4  
F:43-114/Disulfide bonds: #status predicted

Query Match	82.0%;	Score 558.5;	DB 1;	Length 134;
Best Local Similarity	85.4%;	Pred. NO. 1.3e-40;		
Matches 11;	Conservative	6;	Mismatches 12;	Indels 1;
			Gaps	1

**OY**    4 QAOVLILLWVGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTENYLAWYQ 63  
       | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
**Db**    4 QTQVPSLLMLISGAGDIVMTQSPDSLAVSLGERATINCKSSQSILYSDKNKNYLAWYQ 63

```
Qy      64 QKPQPCKLLIYMASTRSGVPDRFSSGSGTFTLTISLQAEDVAVYYCTOSYN-YT 122
        ||||| | | | | | | | | | | | | | | | | | | : |
Db      64 QKPGQPKLLIYCASRSGVPDRFSSGSGTFTLTISLQAEDVAVYYCQYINLPWT 123
```

QY	123	EGQGTKEIK	132
Db	124	EGQGTKEIK	133

RESULT	3
G33932	

19 Kabpa chain precursor V region (U2) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 09-Mar-1990 #sequence-revision 09-Mar-1990 #text-change 21-Jan-2000  
C:Accession: G33932  
R:Baccata, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989  
A:Title: Two murine natural polyclonal autoantibodies are encoded by nonmutated germ line  
I:Reference number: A33932; PMID:89282823

A:Accession: G33932  
A:Status: preliminary; not compared with consensual translation  
A:Molecule type: mRNA  
A:Residues: 1-120 <RAC>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
C:36-116/Domain: immunoglobulin homology <IM>

Query Match	81.9%;	Score 558;	DB 2;	Length 120;
Best Local Similarity	-88.3%;	Pred. NO. 1.3e-40;		
Matches 106; Conservative	8;	Mismatches 6;	Indels 0;	Gaps 0;

[illegible]

RESULT : 4  
S49531  
anti-5m antibody VL chain (V kappa 4/J kappa 3) - human  
C:Species: Homo sapiens (man)

C:Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 21-Jan-2000  
C:Accession: S49531  
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
submitted to the EMBL Data Library, October 1994  
A:Description: Molecular characterization of natural human anti-Sm autoantibodies  
A:Reference number: S48797  
A:Accession: S49531  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-134 <MAH>  
A:Cross-references: EMBL: Z46347; NID: g560841; PIDN: CAA86466.1; PID: g560842  
A:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
F:36-116/Domain: immunoglobulin homology <IMH>

Query Match	81.3%	Score 553.5;	DB 2;	Length 134;
Best Local Similarity	83.1%;	Pred. No. 3.4e-40;		
Matches 108; Conservative	8;	Mismatches 13;	Indels 1;	Gaps 1;

4 QTVFISLLWISGAYGDIVMTPSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQ 63

```

64 QKPGPPKLLIYMASTRESGVDFRSGSGGTDFTLTITSSQLAEADVAVYYCOQYISTFT 123

```

Db 124 FGPSTKVDIK 133

RESULT	5	
KAHUUI		
Ig kappa chain precursor	V-IV region (JI) - human	

C:\date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 21-Jan-2000  
C:\Accession: A01904  
R:\Klobeck, H.G.; Bornkamm, G.W.; Combriato, G.; Mocklat, R.; Pohlenz, H.D.;

A: Nucleic Acids Res. 13, 6515-6529, 1985  
A: Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single gene  
A: Reference number: A93589; MUID:86041853  
A: Accession: A01904  
A: Molecule type: DNA  
A: Residues: 1-133 <K10>  
A: Cross-references: GB:500022; GB:X51570; NID:933158; PIDD:CAAT7317.1; PID:9296654  
A: Note: The sequence was determined from the differentiated gene

C:Genetics:	
A:Gene:	GDB:ICRV
A:Cross-references:	GDB:119341; OMIM:146980
A:Map position:	2p12-2p12
A:Introns:	17/1
C:Complex:	An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into superfamily: immunoglobulin V region; immunoglobulin homology

1-20/Domain: signal sequence #status predicted <SIG>  
21-133/Product: Ig kappa chain V-IV region (JI) #status predicted <MAT>  
21-43/Region: framework 1

F 36-116/Domain: Immunoglobulin homology <IMH>  
F 44-60/Region: complementarity-determining 2  
F 61-75/Region: framework 2  
F 76-82/Region: complementarity-determining 1  
F 83-114/Region: framework 3  
F 115-122/Region: complementarity-determining 3  
F 123-133/Region: framework 4  
F 43-114/Disulfide bonds: #status predicted

Query Match	81.1%;	Score 552;	DB 1;	length 133;
Best Local Similarity	83.7%;	Pred. NO. 4.5e-40;		
Matches 108; Conservative	6;	Mismatches 15;	Indels 0;	Gaps 0;

A:Residues: 1-145 <CHE>  
A:Experimental source: cell line F6-3  
C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphoryl  
C:Superfamily: immunoglobulin V region: immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domin: signal sequence #status predicted <SIG>  
F:21-134/Product: Ig heavy chain V region (CQ1) #status predicted <MAT>  
F:36-116/Domin: immunoglobulin homology <IMM>  
F:44-60/Region: complementarity-determining 1  
F:76-82/Region: complementarity-determining 2  
F:115-123/Region: complementarity-determining 3  
F:135-145/Domin: constant region (fragment) #status predicted <COR>

Query Match 79.5%; Score 541.5; DB 2; Length 145;  
Best Local Similarity 77.6%; Pred. No. 3.8e-39;  
Matches 104; Conservative 18; Mismatches 9; Indels 3; Gaps 2;

OY 1 MDSQAQVILILLIWMSSGCDIVLTQSPDLSAVSGERATISCKSSQLNSRTRENTLA 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 1 MDSQAQVILILLIWMSSGCDIVMSQSPSSSLAVSAGEKVTMSQSOSLILYSNOKNELA 60  
OY 61 WYQOKPGQPKLLIYWASTRESGVDPDRFGSGSGDTFLTITSSLOAEVAVYYCQSYNL 120  
Db 61 WYQOKPGQSPKLLIYWASTRESGVDPDRFTGSQSGDTFLTITSSVAEDLAYVYC-QQYIDS 119

OY 121 Y-TFGQGTKEVEIK 132  
||| |||:-|  
Db 120 YPLTFGSGTKLEMK 133

RESULT 8  
PC1214  
Ig kappa chain precursor V region (mab H8) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PC1214  
R:Hong, H.-J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; K  
Gene 121, 331-335, 1992  
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a  
F:Reference number: PC1213; MUID:93077049  
A:Accession: PC1214  
A:Molecule type: mRNA  
A:Residues: 1-134 <HON>  
A:Cross-references: GB:M8042; NID:g196749; PIDN:AAA38777.1; PID:g196750  
C:Superfamily: immunoglobulin V region: immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domin: signal sequence #status predicted <SIG>  
F:21-134/Product: Ig light chain V region #status predicted <MAT>  
F:36-116/Domin: immunoglobulin homology <IMM>

Query Match 79.2%; Score 539.5; DB 2; Length 134;  
Best Local Similarity 78.9%; Pred. No. 5.2e-39;  
Matches 105; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

OY 1 MDSQAQVILILLIWMSSGCDIVLTQSPDLSAVSGERATISCKSSQLNSRTRENTLA 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 1 MDSQAQVILILLIWMSSGCDIVMSQSPSSSLAVSAGEKVTMSCKSSQSLITSTOKNELA 60  
OY 61 WYQOKPGQPKLLIYWASTRESGVDPDRFGSGSGDTFLTITSSLOAEVAVYYCQSYNL 120  
Db 61 WYQOKPGQSPKLLIYWASTRESGVDPDRFTGSSESDFLTITSNVAEDLAYVYYCQQYYNY 120

OY 121 -YTFGGTKEVEIK 132  
||| |||:||||  
Db 121 PSTFGGTYLEIK 133

RESULT 9  
S38807  
Ig light chain V-J region - mouse  
C:Species: Mus musculus (house mouse)









GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 25, 2001, 09:40:51 : Search time 15.22 Seconds  
(without alignments)  
297.091 Million cell updates/sec

Title: US-09-249-011-8  
Perfect score: 681  
Sequence: 1 MDSQAQVILLILLMWSCGTCG.....YCTOSYNLYTFGOGTKVEIK 132

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 93435 seqs, 3425486 residues  
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571.5	83.9	134	1	P06314
2	552	81.1	133	1	P06313
3	515	75.6	121	1	P06312
4	502.5	73.8	114	1	P06311
5	446	65.5	129	1	P04207
6	442	64.5	129	1	P18135
7	440	64.6	129	1	P18136
8	416.5	61.2	129	1	P06310
9	409.5	60.0	128	1	P06309
10	408.5	60.0	131	1	P06311
11	408.5	60.0	131	1	P06311
12	408.5	60.0	132	1	P06311
13	396	58.1	115	1	P04433
14	394.5	57.9	116	1	P04433
15	394	57.9	110	1	P01668
16	393.5	57.8	136	1	P01634
17	392.5	57.6	149	1	P01633
18	384	56.4	109	1	P01620
19	384	56.4	109	1	P01620
20	383	56.2	109	1	P01622
21	382.5	56.2	111	1	P01665
22	382.5	56.2	111	1	P01667
23	381	55.9	109	1	P01633
24	381	55.9	117	1	P06309
25	380.5	55.9	108	1	P01605
26	380.5	55.9	111	1	P01605
27	379.5	55.7	111	1	P01673
28	379.5	55.7	111	1	P01660
29	375.5	55.1	111	1	P01666
30	374.5	55.0	111	1	P01669
31	374.5	55.0	111	1	P01671
32	374.5	55.0	111	1	P01671
33	373.5	54.8	115	1	P01614

34	370	54.3	109	1	P04206
35	368.5	54.1	117	1	P01602
36	368.5	54.1	129	1	P04432
37	367	53.9	108	1	P01619
38	366.5	53.8	108	1	P01619
39	366.5	53.8	111	1	P04430
40	366.5	53.8	111	1	P03977
41	366.5	53.8	111	1	P01662
42	366.5	53.8	111	1	P01672
43	365.5	53.7	108	1	P01632
44	362.5	53.2	111	1	P01600
45	362	53.2	113	1	P01615

## ALIGNMENTS

RESULT	1	STANDARD	PRT	134 AA.
KVAC_HUMAN				
ID	KVAC_HUMAN			
AC	P06314			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-APR-1988 (Rel. 07, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.			
OS	Homo sapiens (human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
NC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
NC	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86041854; PubMed=2997713;			
RA	Marsh P., Mills F., Gould H.;			
RT	"Detection of a unique human V kappa IV germline gene by a cloned			
RL	cDNA probe."			
RN	Nucleic Acids Res. 13:6531-6544(1985).			
RP	REVISION TO 76.			
RA	Marsh P.;			
RL	Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	EMBL: X02990; CNA26733.1; -			
DR	PIR; A01905; KAHU17.			
DR	HSSP; P01789; ZMCP.			
DR	InterPro; IPR003006; -			
DR	Pfam; PF00047; 19; 1.			
KW	Immunoglobulin V region; Signal.			
FT	STGNL 1 20			
FT	CHAIN 21 134			
FT	DOMAIN 21 43			
FT	DOMAIN 44 60			
FT	DOMAIN 61 75			
FT	DOMAIN 76 82			
FT	DOMAIN 83 114			
FT	DOMAIN 115 121			
FT	DOMAIN 122 133			
FT	DISULFID 43 114			
FT	NON_TER 134			
SO	SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;			

Query Match 83.9%; Score 571.5; DB 1; Length 134;  
Best Local Similarity 86.2%; Pred. No. 3,1e-52;  
Matches 112; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

OY	4	QAOVLILLLWVSGCGIVLTQSPDSLAVSLGERATISCKSSQSGLNSRPRENTLAWQ	63
Dd	4	QTOVFISILLMLTWSGAYGVIMQTQSPDSLAVSLGERATINCKSSQSGLITLVSDMKNTLAWQ	63
OY	64	QKPGPPELLLYMASTRRESGVPDFRRSGSGCTDFTLLTSSLQAEDEVAVYYCTQSYNL-VT	122
Dd	64	QKPGPPELLLYMASTRRESGVPDFRRSGSGCTDFTLLTSSLQAEDEVAVYYCCOQYNLPWT	123
OY	123	FGQGKVEIK	132
Dd	124	FGQGKVEIK	133
<hr/>			
RESULT 2			
ID	KVAB_HUMAN	STANDARD:	PRT: 133 AA.
AC	P06313.		
DT	01-JAN-1988 (Rel. 06, Created)		
DT	01-JAN-1988 (Rel. 06, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	IG KAPPA CHAIN V-IV REGION JI PRECURSOR.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=66041853; PubMed=2997712;		
RA	Klobeck H.G., Bornkamm G.W., Combrlato G., Mocikat R., Pohlenz H.D.,		
RA	Zachau H.G.;		
RT	"Subgroup IV of human immunoglobulin K light chains is encoded by a		
RL	single germ-line gene.";		
CC	Nucleic Acids Res. 13:6515-6529(1985).		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	or send an email to <a href="mailto:license@lsb-sib.ch">license@lsb-sib.ch</a> ).		
CC	-----		
DR	EMBL: Z00022; CAA7317.1; .		
DR	PIR: A01904; KAHUJI.		
DR	HSSP; F01789; ZMCP.		
DR	InterPro; IPR003006; .		
DR	Pfam; PF00047; 19; 1.		
KM	Immunoglobulin V region; Signal.		
FT	SIGNAL	1	20
FT	CHAIN	21	133
FT	DOMAIN	21	43
FT	DOMAIN	44	60
FT	DOMAIN	61	75
FT	DOMAIN	76	82
FT	DOMAIN	83	114
FT	DOMAIN	115	122
FT	DOMAIN	123	132
FT	DISULFID	43	114
FT	NON_TER	133	133
SO	SEQUENCE	133 AA; 14632 MW; 5FB9353066744AF4 CNC64;	
<hr/>			
Query Match 81.1%; Score 552; DB 1; Length 133;			
Best Local Similarity 83.7%; Pred. No. 3,2e+50;			
Matches 108; Conservative 6; Mismatches 15; Indels 0; Gaps 0;			
OY	4	QAOVLILLLWVSGCGIVLTQSPDSLAVSLGERATISCKSSQSGLNSRPRENTLAWQ	63
Dd	4	QTOVFISILLMLTWSGAYGVIMQTQSPDSLAVSLGERATINCKSSQSGLITLVSDMKNTLAWQ	63
OY	64	QKPGPPELLLYMASTRRESGVPDFRRSGSGCTDFTLLTSSLQAEDEVAVYYCTQSYNL-VT	122
Dd	64	QKPGPPELLLYMASTRRESGVPDFRRSGSGCTDFTLLTSSLQAEDEVAVYYCCOQYNLPWT	123
OY	123	FGQGKVEIK	132
Dd	124	FGQGKVEIK	133

[illegible]

DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-IV REGION LEN.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76004342; PubMed=50995;  
 RA Schneider M., Hilschmann N.;  
 RT "The primary structure of a monoclonic immunoglobulin-L-chain of  
 RT subgroup IV of the kappa type (Bence-Jones protein len.).";  
 RL Hope-Seyler's Z. Physiol. Chem. 356:507-557(1975).  
 RN [2]  
 RP REVISION TO 9.  
 RA Salomon A.;  
 RL Submitted (AUG-1996) to the SWISS-PROT data bank.  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.  
 DR PIR: A01903; K4HUN.  
 DR HSSP: P01789; 2MCP.  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; 19; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 2 41 55 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 3 56 62 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 4 63 94 FRAMEWORK 3.  
 FT DOMAIN 5 95 101 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 6 102 113 FRAMEWORK 4.  
 FT DISULFID 23 94 BY SIMILARITY.  
 FT NON\_TER 114 114  
 SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17E236485 CRC64;  
  
 Query Match 73.8%; Score 502.5; DB 1; Length 114;  
 Best Local Similarity 86.7%; Pred. No. 3.4e-45;  
 Matches 98; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
  
 QY 21 DIVTQSPDLAVSLGERATISCKSSQSLNSTRRENYLAWYQKPGPKLLIYASTR 80  
 DB 1 DIVTQSPDLAVSLGERATISCKSSQSLNSTRRENYLAWYQKPGPKLLIYASTR 60  
 QY 81 ESGVDPFRSGSGSGDTFTLTISLQAEADVAVVYCTOSYNL-YTFGGCTKVEIK 132  
 DB 61 ESGVDPFRSGSGSGDTFTLTISLQAEADVAVVYCTOSYNL-YTFGGCTKLEIK 113  
  
 RESULT 5  
 KVAL\_HUMAN  
 ID KVAL\_HUMAN STANDARD; PRT; 129 AA.  
 AC P04207;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION CLL PRECURSOR (RHEUMATOID FACTOR).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86177570; PubMed=3083417;  
 RA Jirik F.R., Sorge J., Fong S., Heltzmann J.G., Cud J.G., Chen P.P.,  
 RA Goldfine R., Carson D.A.;  
 RT "Cloning and sequence determination of a human rheumatoid factor  
 RT light-chain gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 OX EMBL: M12740; AAA58992.1; -  
 DR PIR: A01898; K3HUNL.  
 DR HSSP: P01789; 2MCP.  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; 19; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.  
 FT DOMAIN 1 21 43 FRAMEWORK 1.  
 FT DOMAIN 2 44 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 3 55 69 FRAMEWORK 2.  
 FT DOMAIN 4 70 76 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 5 77 108 FRAMEWORK 3.  
 FT DOMAIN 6 109 118 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 7 119 129 JK1 SEGMENT.  
 FT DISULFID 43 108 BY SIMILARITY.  
 FT NON\_TER 129 129  
 SQ SEQUENCE 129 AA; 14275 MW; 5C13BA11BB60CC14 CRC64;  
  
 Query Match 65.5%; Score 446; DB 1; Length 129;  
 Best Local Similarity 66.7%; Pred. No. 2.7e-39;  
 Matches 90; Conservative 20; Mismatches 15; Indels 10; Gaps 3;  
  
 QY 1 MSDQAVLILLLVSGDSIVLTQSPDSLAVSLGERATISCKSSQSLNSTRRENYLA 60  
 DB 1 MSDQAVLILLLVSGDSIVLTQSPDSLAVSLGERATISCKSSQSLNSTRRENYLA 54  
 QY 61 WYQKPGPKLLIYASTRSGVDPFRSGSGSGDTFTLTISLQAEADVAVVYCTOSYN- 119  
 DB 55 WYQKPGPKLLIYASTRSGVDPFRSGSGSGDTFTLTISLQAEADVAVVYCTOSYN- 113  
 QY 120 --LYTFGGCTKVEIK 132  
 DB 114 WPTWFGGCTKVEIK 128  
  
 RESULT 6  
 KVAL\_HUMAN  
 ID KVAL\_HUMAN STANDARD; PRT; 129 AA.  
 AC P18135;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88171307; PubMed=3127527;  
 RA Kips T.J., Tomhave E., Chen P.P., Carson D.A.;  
 RT "Antenatally-associated kappa light chain variable region gene  
 RT expressed in chronic lymphocytic leukemia with little or no somatic  
 RT mutation. Implications for etiology and immunotherapy.";  
 RL J. Exp. Med. 167:840-852(1988).  
 CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M  
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC  
 CC LEUKEMIA.  
 DR PIR: P10022; K3HUNL.  
 DR HSSP: P01789; 2MCP.  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; 19; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.

FT DOMAIN 21 43 FRAMEWORK 1.  
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 56 70 FRAMEWORK 2.  
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 78 109 FRAMEWORK 3.  
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 119 129 JKI SEGMENT.  
FT DISULFID 43 109 BY SIMILARITY.  
FT NON\_TER 129 129  
SO SEQUENCE 129 AA; 14073 MM; D3C55292772774D0 CRC64;

Query Match 64.9%; Score 442; DB 1; Length 129;  
Best Local Similarity 66.9%; Pred. No. 7e-39;  
Matches 89; Conservative 19; Mismatches 19; Indels 6; Gaps 2;

OY 1 MDSQAQVILLILLWVSGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRRENTLYA 60  
DB 1 METPQQLFLILLMLPDTTGEIVLTQSPGTLISLSPGERATLSCRASQSVSSS-----YLA 55

OY 61 WYQKPGQPKLLIYMASTRSGVDPDRFSGSGSGTDFTLTSSLAQEDVAVYYCTQ-SYN 119  
DB 56 WYQKPGQAPRLIYGAASSRATGIPDRFSGSGSGTDFTLTSLRLPEDPFAVYYCQYQYTS 115

OY 120 LYTFGQGTKEIK 132  
DB 116 PRTFGQGTKEIK 128

RESULT 7  
KV3M\_HUMAN STANDARD; PRT; 129 AA.  
AC P18136;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88171307; PubMed=3127527;  
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
RT "Autoantibody-associated kappa light chain variable region gene  
mutation expressed in chronic lymphocytic leukemia with little or no somatic  
mutation. Implications for etiology and immunotherapy.";  
RL J. Exp. Med. 167:840-852(1988).  
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M  
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC  
LEUKEMIA.  
CC PIR: P10021; K3HUII.  
DR HSSP: P01789; 2MCP.  
DR InterPro: IPR003006;  
DR Pfam: PF00047; 19; 1.  
KW Immunoglobulin V region; Signal.  
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.  
FT DOMAIN 21 43 FRAMEWORK 1.  
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 56 70 FRAMEWORK 2.  
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 78 109 FRAMEWORK 3.  
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 119 129 JKI SEGMENT.  
FT DISULFID 43 109 BY SIMILARITY.  
FT NON\_TER 129 129  
SO SEQUENCE 129 AA; 14070 MM; 7395528EA2BB74D6 CRC64;

Query Match 64.6%; Score 440; DB 1; Length 129;  
Best Local Similarity 66.2%; Pred. No. 1.1e-38;

Matches 88; Conservative 20; Mismatches 19; Indels 6; Gaps 2;

OY 1 MDSQAQVILLILLWVSGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRRENTLYA 60  
DB 1 METPQQLFLILLMLPDTTGEIVLTQSPGTLISLSPGERATLSCRASQSVSSS-----YLA 55

OY 61 WYQKPGQPKLLIYMASTRSGVDPDRFSGSGSGTDFTLTSSLAQEDVAVYYCTQ-SYN 119  
DB 56 WYQKPGQAPRLIYGAASSRATGIPDRFSGSGSGTDFTLTSLRLPEDPFAVYYCQYQYTS 115

OY 120 LYTFGQGTKEIK 132  
DB 116 PRTFGQGTKEIK 128

RESULT 8  
KV2E\_HUMAN STANDARD; PRT; 133 AA.  
AC P06310;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-II REGION RPMI 6410 PRECURSOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86041852; PubMed=2997711;  
RA Klobbeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;  
RT "Human immunoglobulin kappa light chain genes of subgroups II and  
III.";  
RL Nucleic Acids Res. 13:6499-6513(1985).  
CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: Z00020; CAAT7315.1; -;  
DR PIR: A01890; K2HURP.  
DR InterPro: IPR003006;  
DR Pfam: PF00047; 19; 1.  
KW Immunoglobulin V region; Signal.  
FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.  
FT DOMAIN 21 43 FRAMEWORK 1.  
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 60 74 FRAMEWORK 2.  
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 82 113 FRAMEWORK 3.  
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 123 132 FRAMEWORK 4.  
FT DISULFID 43 113 BY SIMILARITY.  
FT NON\_TER 133 133  
SO SEQUENCE 133 AA; 14707 MM; 513CCAFA3673009EE CRC64;

Query Match 61.4%; Score 418; DB 1; Length 133;  
Best Local Similarity 65.9%; Pred. No. 2.2e-36;  
Matches 85; Conservative 19; Mismatches 23; Indels 2; Gaps 2;

OY 5 AQLGLILLWVSGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRRENTLYA 64  
DB 5 AQLGLILLWVSGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRRENTLYA 64

OY 65 KPGQPKLLIYMASTRSGVDPDRFSGSGSGTDFTLTSSLAQEDVAVYYCTQ-SYN 123  
DB 64 KPGQPKLLIYKVSRRDGVDPDRFSGSGSGTDFTLTSLRVEADVAVYYCQGTHTSWTF 123

OY 124 GOSTKVEIK 132  
 DB 124 GOSTKVEIK 132

## RESULT 9

KV3K\_HUMAN

STANDARD: PRT: 129 AA.

ID

KV3K\_HUMAN

AC

P04431;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION WALKER PRECURSOR.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85014148; PubMed=6091049;

RA Klobbeck H.G.; Combrato G.; Zachau H.G.;

RT Immunoglobulin genes of the kappa light chain type from two human

RL Nucleic Acids Res. 12:6995-7006(1984).

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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: X00965; CAA25477.1; ALT\_TERM.

DR PIR: A01883; K1HWK.

DR HSSP: P01607; 1REI.

DR InterPro: IPR003006; .

DR Pfam: PF00047; 19; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 22

FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.

FT DOMAIN 23 45 FRAMEWORK 1.

FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 57 71 FRAMEWORK 2.

FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 79 110 FRAMEWORK 3.

FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 120 129 FRAMEWORK 4.

FT DISULFID 45 110 BY SIMILARITY.

FT NON\_TER 129 129

SO SEQUENCE 129 AA; 14069 MW; P941FA07DAAFC2P9 CRC64;

Query Match 61.2%; Score 416.5; DB 1; Length 129;  
 Best Local Similarity 65.9%; Pred. No. 3e-36;  
 Matches 85; Conservative 16; Mismatches 21; Indels 7; Gaps 2;

OY 5 AOVLLILLVWSTGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLAQQ 64  
 DB 7 AQLGLLLMLRGARCDIQMTQSPSSLSASVGRVITTCASOSI-----SNVLNMQQ 60

OY 65 KRQAPKLLIYMASTRESGVDPDRFSGSGGTFTLTSSIAQAEVAVYYCTOSYN-LYTF 123  
 DB 61 KPRKAPKLLIYMASTRESGVDPDRFSGSGGTFTLTSSIAQAEVAVYYCTOSYN-LYTF 120

OY 124 GOSTKVEIK 132  
 DB 121 GOSTKVEIK 129

## RESULT 10

KV3K\_HUMAN

ID KV3K\_HUMAN STANDARD: PRT: 128 AA.

AC P06311;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86041852; PubMed=2997711;

RA Klobbeck H.G.; Meindl A.; Combrato G.; Solomon A.; Zachau H.G.;

RT Human immunoglobulin kappa light chain genes of subgroups II and

RL Nucleic Acids Res. 13:6499-6513(1985).

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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: Z00021; CAA77316.1; .

DR PIR: A01899; K3H041.

DR InterPro: IPR003006; .

DR Pfam: PF00047; 19; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.

FT DOMAIN 21 43 FRAMEWORK 1.

FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 55 69 FRAMEWORK 2.

FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 77 108 FRAMEWORK 3.

FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 118 128 JKI SEGMENT.

FT DISULFID 43 108 BY SIMILARITY.

FT NON\_TER 128 128

SO SEQUENCE 128 AA; 14070 MW; CC895780FEB9012 CRC64;

Query Match 60.1%; Score 409.5; DB 1; Length 128;  
 Best Local Similarity 63.2%; Pred. No. 1.6e-35;  
 Matches 84; Conservative 21; Mismatches 21; Indels 7; Gaps 2;

OY 1 MDSQAVLILLVWSTGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60  
 DB 1 MESPQAVLILLVWSTGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 54

OY 61 WYQKRPQPKLLIYMASTRESGVDPDRFSGSGGTFTLTSSIAQAEVAVYYCTQ-SYN 119  
 DB 55 WYQKRPQPKLLIYMASTRESGVDPDRFSGSGGTFTLTSSIAQAEVAVYYCTQ-SYN 114

OY 120 LYTFGOSTKVEIK 132  
 DB 115 PYTFGOSTKVEIK 127

## RESULT 11

KV3L\_MOUSE

KV3L\_MOUSE

ID KV3L\_MOUSE STANDARD: PRT: 131 AA.

AC P01661;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN (2)
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKeane D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN (3)
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKeane D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KWSM6.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 60.0%; Score 408.5; DB 1; Length 131;
Best Local Similarity 62.4%; Pred. No. 2e-35;
Matches 83; Conservative 21; Mismatches 26; Indels 3; Gaps 2;

OY 1 MDSQAOVILLLWVSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENTLA 60
DB 1 METDILLWVLLWVPGSTGIVLTQSPASLAVALSGORATISCRASESV--DSYGNSTFMH 58
OY 61 WYQKPGQPKLLIYMASTRSGVDPDRFSGSGSGTDFTLTISLQAEDVAVYYCTQ--SYN 119
DB 59 WYQKPGQPKLLIYRASNLGSGVAPRRSGSGSRDFTLTIDPVADDAATFYCCQNNMD 118
OY 120 LYTEGGQTKVEIK 132
DB 119 PWTEGGGTKLEIK 131

RESULT 12
KV3F_MOUSE STANDARD: PRT; 132 AA.
AC P01653;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 321 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE OF 1-37.

```

```

RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN (2)
RP SEQUENCE OF 21-132.
RX MEDLINE=73140224; PubMed=4120629;
RA McKeane D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
RT chain.";
RL Biochemistry 12:749-759(1973).
CC -I- MISCELLANEOUS: "THE PARTIAL SEQUENCE OF THE C REGION OF THIS
CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
CC REPORTED FOR MOUSE MORE 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
CC RESIDUES."
DR PIR; A01933; KWS32.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; 19; 1.
KW Immunoglobulin V region; Bence-Jones protein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 132 IG KAPPA CHAIN V-III REGION MOPC 321.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FBE9 CRC64;

Query Match 60.0%; Score 408.5; DB 1; Length 132;
Best Local Similarity 58.6%; Pred. No. 2.1e-35;
Matches 78; Conservative 28; Mismatches 24; Indels 3; Gaps 2;

OY 1 MDSQAOVILLLWVSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENTLA 60
DB 1 METDILLWVLLWVPGSTGIVLTQSPASLAVALSGORATISCRASKSV--NTYGNSTFMZ 58
OY 61 WYQKPGQPKLLIYMASTRSGVDPDRFSGSGSGTDFTLTISLQAEDVAVYYCTQS--YN 119
DB 59 WYZZKPGQPKLLIYRASNLGSGVAPRRSGSGSRDFTLTIDPVZABDVATFYCCZSSBZ 118
OY 120 LYTEGGQTKVEIK 132
DB 119 PWTEGGGTKLEIK 131

RESULT 13
KV3I_HUMAN STANDARD: PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION VG PRECURSOR (FRAMEWORK).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the YK locus";
RL Nucleic Acids Res. 12:9229-9236(1984).
CC -----

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Mon Apr 30 07:08:35 2001

us-09-249-011-8.rsp

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Search completed: April 25, 2001, 09:40:51  
Job time: 176 sec

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Query Match	55.78;	Score 379;	DB 4;	Length 109;
Best Local	68.18;	Pred. No. 4.7e-33;		
Similarity				

RESULT	5			
090UL70				
ID				
AC	090UL70	PRELIMINARY;	PRT;	108 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	MOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT)			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; PubMed=9614993;			
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	tetus.";			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			



```

RESULT 9
Q9UL80 ID 09UL80 PRELIMINARY; PRT: 114 AA.
AC 09UL80:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
DR Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035034; AAD56270.1; -.
DR INTERPRO: IPR003006; -.
DR PIRAF: PF00047; 19; 1.
FT NON_TER 1 1
FT 114 114
SEQUENCE 114 AA; 12775 MW; 070E31E210DICB01 CRC64;

Query Match
Best Local Similarity 51.8%; Score 352.5; DB 4; Length 114;
Matches 73; Conservative 15; Mismatches 23; Indels 3; Gaps 2;

Db 1 DVMQOSLSLPVILROKASISCRSSQSPVYS-DCNTILNMFQOPRPGSPRLIYKVSNR 59
QY 81 EGVGPDRESGSGGTDTLTITSSLOAEDVAVYCTQS--YVLYTFGGCTKVEIK 132
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 DSGVDFRSGSGGTDTLTITSSLOAEDVAVYCTQS--YVLYTFGGCTKVEIK 113

RESULT 10
Q9JL82 ID 09JL82 PRELIMINARY; PRT: 104 AA.
AC 09JL82:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206024; AAF69322.1; -.
FT NON_TER 1 1
FT 104 104
SEQUENCE 104 AA; 11360 MW; 5DA8BBF5FOAIAAE CRC64;

Query Match
Best Local Similarity 50.1%; Score 341; DB 11; Length 104;
Matches 69; Conservative 16; Mismatches 17; Indels 2; Gaps 2;

Db 30 SLAVSLGERATISCKSSQSLNSRRENTLAWYQKPGQPKLLIYMASTRSGVPPDRFS 89

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Db 2 SLVPSLGDQASISCRSSQSLVHT-NGNTYLHMYLQKPGQSPKLLIYKVSNNRSGVPPDRFS 60
QY 90 GSGSGTDFLTITSSLOAEDVAVYCTQSYNL-YTFGGCTKVEIK 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GSGSGTDFLTITSSLOAEDVAVYCTQSYNL-YTFGGCTKVEIK 104

RESULT 11
Q9JL74 ID 09JL74 PRELIMINARY; PRT: 99 AA.
AC 09JL74:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206032; AAF69330.1; -.
FT NON_TER 1 1
FT 99 99
SEQUENCE 99 AA; 10939 MW; 3B25D0E7B453324 CRC64;

Query Match
Best Local Similarity 49.4%; Score 336.5; DB 11; Length 99;
Matches 67; Conservative 14; Mismatches 15; Indels 7; Gaps 2;

Db 3 LLVSGADRVITTKAKSQSVND-----VAVYQKPGQSPKLLIYASNRITGVPPDRFTG 56
QY 91 SSGSGTDFLTITSSLOAEDVAVYCTQSYNL-YTFGGCTKVEIK 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 SSGSGTDFLTITSSLOAEDVAVYCTQSYNL-YTFGGCTKVEIK 99

RESULT 12
Q9RIAS ID 09RIAS PRELIMINARY; PRT: 214 AA.
AC 09RIAS:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Kramadouliah A.K.M., Mitra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152371; AAD40242.1; -.
DR HSSP: P01789; IMCP.
DR INTERPRO: IPR003006; -.
DR PIRAF: PF00047; 19; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1 1
FT 214 214
SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

```

Query Match 48.7%; Score 331.5; DB 11; Length 214;  
 Best Local Similarity 58.4%; Pred. No. 1.2e-27;  
 Matches 66; Conservative 16; Mismatches 24; Indels 7; Gaps 2;

QY 21 DIVLQSPDSLAVSLGERATISCKSSQSLNSRTRENTYLAWYQKPGPKLLIYWA5TR 80  
 1 DLQLTQSPSMAVSLGERATITCKASQDI-----NSYLSMFQKPGKSPKLLIYANRL 54

DB 81 ESGVPRFSGSGSDTFTLTISLQAEADVAVYCTQSYNL-YTFGGGTVEIK 132  
 55 VGVGPRFSGSGSDYSLTISLSEYEDMGVICYQYDERFFTFGGGTLEIK 107

RESULT 13  
 Q9JL80 PRELIMINARY; PRT; 103 AA.

AC Q9JL80; PRELIMINARY; PRT; 103 AA.  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C;  
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-  
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis."  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF206026; AAF69324.1;  
 FT NON\_TER 1 103  
 FT SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

Query Match 47.7%; Score 324.5; DB 11; Length 103;  
 Best Local Similarity 63.5%; Pred. No. 2.8e-27;  
 Matches 66; Conservative 17; Mismatches 18; Indels 3; Gaps 2;

QY 30 SLAVSLGERATISCKSSQSLNSRTRENTYLAWYQKPGPKLLIYWA5TRSGVDPRES 89  
 2 SLAVSLGORTATISCRASESEYVYGT--SLMQWYQKPGPKLLIYAASNVESGVPARFS 59

DB 90 GSGSGTDFLTISLQAEADVAVYCTQSYNL-YTFGGGTVEIK 132  
 60 GSGSGTDFSLNHPVEDDIAMFCQSKRVPTFGGTLEIK 103

RESULT 14  
 Q9NP29 PRELIMINARY; PRT; 130 AA.

AC Q9NP29; PRELIMINARY; PRT; 130 AA.  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE MICROFILBRILAR PROTEIN 2 (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=96354815; PubMed=8753791;  
 RA Ozsvath K.J., Xia S., Hirose H., Tilsen M.D.;  
 RT "Two hypothetical proteins of human aortic adventitia, with 1g kappa,  
 collagenous, and aromatic-rich motifs."  
 RL Biochem. Biophys. Res. Commun. 225:500-504(1996).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=97367690; PubMed=9224393;  
 RA Ozsvath K.J., Hirose H., Xia S., Chew D., Knoetgen J. III,  
 RA Tilsen M.D.;  
 RT "Expression of two novel recombinant proteins from aortic adventitia  
 (kappa1b3) sharing amino acid sequences with cyclomegalovirus."  
 RL J. Surg. Res. 69:277-282(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Ozsvath K.J., Xia S., Hirose H., Tilsen M.D.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF206020; AAF62402.1;  
 FT NON\_TER 130  
 FT SEQUENCE 130 AA; 14128 MW; 51275185ACC6FALE CRC64;

Query Match 46.8%; Score 319; DB 4; Length 130;  
 Best Local Similarity 69.2%; Pred. No. 1.4e-26;  
 Matches 63; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 4 QAVLILLILWVGTDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENTYLAWY 63  
 4 QTVFSLILWISGAMGDIVLTQSPDSLAVSLGERATINCRSSORLFGSNSKNYLAWY 63

DB 64 QKPGPKLLIYWA5TRSGVDPRESGSG 94  
 64 QKPGPKLLIYWA5TRSDSVLTSLAGLG 94

RESULT 15  
 Q9QYF0 PRELIMINARY; PRT; 298 AA.

AC Q9QYF0; PRELIMINARY; PRT; 298 AA.  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE CN 8 SCFV.  
 GN CN 8.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE=SPLEEN.  
 RA Shinohara N., Demura T., Fukuda H.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE=SPLEEN.  
 RA Shinohara N., Demura T., Fukuda H.;  
 RT "Isolation of a novel type of vascular cell wall-specific monoclonal  
 antibody recognizing a cell polarity using a phage display subtraction  
 method."  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB036341; BAA88633.1;  
 DR HSSP; P01607; IREI.  
 DR INTERPRO; IPR003006;  
 DR PIRAM; PF00047; I9; 2.  
 SO SEQUENCE 298 AA; 31867 MW; E0F96BBA17004317 CRC64;

Query Match 46.3%; Score 315.5; DB 11; Length 298;  
 Best Local Similarity 55.6%; Pred. No. 9e-26;  
 Matches 65; Conservative 15; Mismatches 30; Indels 7; Gaps 2;

QY 17 GTGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENTYLAWYQKPGPKLLIY 76  
 169 GGSDELTLTQSPDSLAVSEVETITCRASGNT-----HNYLAWYQKPGPKLLIY 222

DB 77 ASTRESVPRFSGSGSDTFTLTISLQAEADVAVYCTQSYNL-YTFGGGTVEIK 132  
 223 AKTLADGVPRFSGSGSDYSLTISLSEYEDMGVICYQYDERFFTFGGGTLEIK 279

Search completed: April 25, 2001, 09:40:34  
Job time: 199 sec

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[illegible][illegible]



Db 121 ytfgggtkleik 132

## RESULT 3

P93078 standard; peptide: 148 AA.

AC P93078;

DT 14-MAR-1990 (first entry)

DE Light chain of monoclonal antibody 6A4.

KW Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.

PN EP338395-A.

PD 25-OCT-1989.

PF 12-APR-1989; 89EP-0106463.

PR 19-APR-1988; 88DE-3813023.

PA (BEHM) BEHRINGWERKE.

PI Domdey H, Marget M, von Specht BU;

DR WPI, 1989-310861/43.

DR N-PSDB; N91663.

PT Monoclonal antibody to Pseudomonas aeruginosa and DNA coding for

PS variable antibody regions.

XX Claim 1; page 6; 7pp; german.

CC The peptide is encoded by the light chain of monoclonal antibody 6A4.

CC 6A4 reacts with the OMP-1 protein of all 19 known serotypes of

CC P.aeruginosa. It is used for therapy and diagnosis of infection, and as

CC a carrier for drugs. The antibody is IgG2a subclass.

CC Sequence 148 AA;

SO Query Match 87.5%; Score 596; DB 10; Length 148;

Best Local Similarity 86.4%; Pred. No. 2.1e-40; Mismatches 8; Indels 0; Gaps 0;

Matches 114; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDSQAOVLILLVMSGTCGDIYLTOSPSLAVSLGERATISCKSSQSLNSRTRENYLA 60

Db 1 mdsqagvlllllllwsqtcgdilwmsqpslavsagekvmsckssqslinslrknfla 60

QY 61 WYQOKFGQPKLLIYMASTRSGVPRFSGSGGTFDTLTISLQADVAVYCTOSYNL 120

Db 61 wyqkpgsgpkllywastresgvpdrftlsgsgtdftlissvgaedlaivckqsytl 120

QY 121 YTFGQGTKEIK 132

Db 121 rtfgggtkleik 132

RESULT 4

R76087 standard; Protein: 239 AA.

AC R76087;

DT 21-NOV-1995 (first entry)

DE MAb 55.1 light chain.

XX Antigen binding structure; complementarity determining region; CDR;

KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;

KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;

KW transgenic animal; transgenic plant; antibody engineering;

KW humanized antibody; immunotoxin.

OS Mus sp.

XX Key

FT Peptide

FT Protein

FT Protein

FT Protein

XX W09515382-A.

PD 08-JUN-1995.

PF 29-NOV-1994; 94WO-GB02610.

PR 03-JUN-1994; 94GB-0011089.

PR 03-DEC-1993; 93GB-0024819.

PA (ZENEC) ZENEC LTD.

PI Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;

PI Rose MS, Wright AF;

DR WPI, 1995-215262/28.

DR N-PSDB; Q94036.

XX Antigen binding structures containing CDRs recognising the CA55.1

XX antigen - produced by hybridomas and host cells, for use in the

XX diagnosis and therapy of cancer

XX Disclosure; Fig.16; 121pp; English.

XX MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated

XX CC chains of 55.1. cDNAs for the heavy (Q94037) and light (Q94036)

XX CC chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scfv or

XX CC Y-mim humanized 55.1 constructs have been expressed in myeloma

XX CC cells and E. coli.

XX Sequence 239 AA;

SO Query Match 86.9%; Score 592; DB 16; Length 239;

Best Local Similarity 84.8%; Pred. No. 7e-40; Mismatches 9; Indels 0; Gaps 0;

Matches 112; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDSQAOVLILLVMSGTCGDIYLTOSPSLAVSLGERATISCKSSQSLNSRTRENYLA 60

Db 1 mdsqagvlllllllwsqtcgdilwmsqpslavsagekvmsckssqslinslrknfla 60

QY 61 WYQOKFGQPKLLIYMASTRSGVPRFSGSGGTFDTLTISLQADVAVYCTOSYNL 120

Db 61 wyqkpgsgpkllywastresgvpdrftlsgsgtdftlissvgaedlaivckqsytl 120

QY 121 YTFGQGTKEIK 132

Db 121 rtfgggtkleik 132

## RESULT 5

W10545 standard; Protein: 137 AA.

AC W10545;

DT 25-SEP-1997 (first entry)

DE Humanised murine anti-E-selectin antibody Cy1788V(LB).

XX Humanised; murine; mouse; E-selectin; antibody; light chain;

KW variable region; detection; inhibition; mediation; cell adhesion;  
KW diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;  
KW acute respiratory distress syndrome; gross cystic breast disease;  
KW cancer; treatment; splanchnic occlusion shock; psoriasis;  
KW complement; chimeric.  
XX  
OS Chimeric - Mus spp.  
OS Chimeric - Homo sapiens.  
OS Synthetic.  
XX  
PN WO9640942-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US09204.  
XX  
PR 07-JUN-1995; 95US-0482112.  
XX  
PA (CYTE-) CYTEL CORP.  
XX  
PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;  
PI Jones S;  
XX  
DR WPI: 1997-077272/07.  
DR N-PSDB: T60730.  
XX  
XX  
XX Humanised anti-E-selectin antibody - useful for diagnosis and  
PT treatment of, e.g. inflammatory responses, septic shock, acute  
PT respiratory distress syndrome or cancer  
XX  
PS Claim 18; Page 71; 89pp; English.  
XX  
XX The present sequence is the humanised murine anti-E-selectin  
CC antibody (Ab) light chain variable region, CY1788V(LA). The Ab can  
CC be used to detect E-selectin, or inhibit E-selectin mediated cell  
CC adhesion. It can also be used to diagnose, reduce or inhibit an  
CC inflammatory response, or the severity of pathologies, e.g. septic  
CC shock, acute respiratory distress syndrome, wound associated  
CC sepsis, gross cystic breast disease or cancer, or treat, e.g.  
CC splanchnic occlusion shock, or psoriasis. It can be administered to  
CC a human without inducing an immune response, in addition, the  
CC effector portion of the Ab can interact with various components of  
CC the human immune system, including complement.  
XX  
SQ Sequence 137 AA:  
  
Query Match 85.2%; Score 580.5; DB 18; Length 137;  
Best Local Similarity 85.0%; Pred. No. 3.3e-39;  
Matches 113; Conservative 8; Mismatches 11; Indels 1; Gaps 1;  
  
QY 1 MDSQAQVLLILLMWSGTGDIVLTQSPDSLAVSLGERATISCKSSQSILNSRTRENTLA 60  
Db 5 mesqfqlvmsllflwsgtgcgdvltmqtspslavslgeratlnckssqslhnsqknylt 64  
QY 61 WYQQRGCPKPKLLIYWASTRRESGVDPDRFGSGSGGTFTLTISLQAEVAVYVCQSYNL 120  
Db 65 WYQKPGQPKPKLLIYWASTRRESGVDPDRFGSGSGGTFTLTISLQAEVAVYVCQSYNL 124  
QY 121 -YTFGQGTKEIK 132  
Db 125 pltfqggtkveik 137  
  
RESULT 6  
ID W10544  
XX W10544 standard; Protein: 137 AA.  
AC W10544;  
XX  
DT 25-SEP-1997 (first entry)  
XX  
DE Humanised murine anti-E-selectin antibody CY1788V(LA).

XX Humanised; murine; mouse; E-selectin; antibody; light chain;  
KW variable region; detection; inhibition; mediation; cell adhesion;  
KW diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;  
KW acute respiratory distress syndrome; gross cystic breast disease;  
KW cancer; treatment; splanchnic occlusion shock; psoriasis;  
KW complement; chimeric.  
XX  
OS Chimeric - Mus spp.  
OS Chimeric - Homo sapiens.  
OS Synthetic.  
XX  
PN WO9640942-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US09204.  
XX  
PR 07-JUN-1995; 95US-0482112.  
XX  
PA (CYTE-) CYTEL CORP.  
XX  
PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;  
PI Jones S;  
XX  
DR WPI: 1997-077272/07.  
DR N-PSDB: T60729.  
XX  
XX  
XX Humanised anti-E-selectin antibody - useful for diagnosis and  
PT treatment of, e.g. inflammatory responses, septic shock, acute  
PT respiratory distress syndrome or cancer  
XX  
PS Claim 17; Page 69; 89pp; English.  
XX  
XX The present sequence is the humanised murine anti-E-selectin  
CC antibody (Ab) light chain variable region, CY1788V(LA). The Ab can  
CC be used to detect E-selectin, or inhibit E-selectin mediated cell  
CC adhesion. It can also be used to diagnose, reduce or inhibit an  
CC inflammatory response, or the severity of pathologies, e.g. septic  
CC shock, acute respiratory distress syndrome, wound associated  
CC sepsis, gross cystic breast disease or cancer, or treat, e.g.  
CC splanchnic occlusion shock, or psoriasis. It can be administered to  
CC a human without inducing an immune response, in addition, the  
CC effector portion of the Ab can interact with various components of  
CC the human immune system, including complement.  
XX  
SQ Sequence 137 AA:  
  
Query Match 84.5%; Score 575.5; DB 18; Length 137;  
Best Local Similarity 84.2%; Pred. No. 8.2e-39;  
Matches 112; Conservative 8; Mismatches 12; Indels 1; Gaps 1;  
  
QY 1 MDSQAQVLLILLMWSGTGDIVLTQSPDSLAVSLGERATISCKSSQSILNSRTRENTLA 60  
Db 5 mesqfqlvmsllflwsgtgcgdvltmqtspslavslgeratlnckssqslhnsqknylt 64  
QY 61 WYQQRGCPKPKLLIYWASTRRESGVDPDRFGSGSGGTFTLTISLQAEVAVYVCQSYNL 120  
Db 65 WYQKPGQPKPKLLIYWASTRRESGVDPDRFGSGSGGTFTLTISLQAEVAVYVCQSYNL 124  
QY 121 -YTFGQGTKEIK 132  
Db 125 pltfqggtkveik 137  
  
RESULT 7  
ID Y95243  
XX Y95243 standard; Protein: 137 AA.  
AC Y95243;  
XX  
DT 29-AUG-2000 (first entry)  
XX

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XX Humanised antibody HuCC49 light chain variable region.
DE
XX
XX Humanised antibody; monoclonal antibody; CC49; HuCC49; CDR;
KW complementarity determining region; mouse; human; carcinoma;
KW colon cancer; tumor associated glycoprotein-72; TAG-72;
XX tumour marker; diagnosis; therapy.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 44..59
FT /note= "CDR1"
FT Region 76..82
FT /note= "CDR2"
FT Region 115..123
FT /note= "CDR3"
XX
PN WO200026394-A1.
XX
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US25552.
XX
XX 31-OCT-1998; 98US-0106534.
XX
XX 02-NOV-1998; 98US-0106757.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kashmiri SVS, Padlan EA, Schlom J;
XX
XX WPI; 2000-365637/31.
XX
XX Chimeric variants of CC49 monoclonal antibodies useful for detecting
XX and treating cancers associated with the expression of the pancreaticoma
XX tumor-associated antigen TAG-72 -
XX
XX Disclosure; Fig 4; 76pp; English.
XX
XX The present sequence is that of the light chain variable region
XX (VL) of huCC49, a humanised monoclonal antibody (MAB) formed by
XX grafting hypervariable regions from murine Mab CC49 into VL and VH
XX frameworks of human Mabs LEN and 21/28' CL, respectively, while
XX retaining murine framework residues required for integrity of the
XX antigen combining site structure. HuCC49 binds to the human
XX pancreaticoma tumor associated glycoprotein-72 (TAG-72), which is
XX found on the surface of certain human tumours. The invention is
XX directed towards mouse-human chimeric variants of CC49 Mabs with
XX minimal murine content, to methods of making such variants, and
XX their therapeutic application. The invention provides
XX complementarity determining region (CDR) variants of huCC49 in
XX which fewer than all 6 CDRs of CC49 are present, and specifically
XX determining region (SDR) variants of huCC49 in which only SDRs of
XX at least 1 CDR from CC49 are present. Particular variants of HuCC49
XX have either L-CDR1 and/or L-CDR2 from human MAB LEN. These
XX variants have the same or 2-fold lower affinity constant than
XX huCC49. Other variants additionally have corresponding human
XX residues at position 97 of L-CDR3, and positions 60, 61, 62 and 64
XX of H-CDR2. The variants are used in claimed methods of treating
XX cancer and for detecting cancer cells that express TAG-72.
XX
SQ Sequence 137 AA;

```

```

Query Match      83.3%; Score 567.5; DB 21; Length 137;
Best Local Similarity 82.7%; Pred. No. 3.5e-38;
Matches 110; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

```

```

QY 1 MDSQAOVLILLVSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 mdsqagvllmlllhwsgtgdilvmsgspdsavslgervtlcnksqsllysgnkyia 60

```

```

QY 61 WYQOKPGOPPKLLIYMASTRSGVDPDRFSGSGGTFTLTITSSLOAEDVAVYCTOSYNL 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 wygqkpgpspklllywasaresyvpdrfsgsggtftltitssvgaedvayycqyysy 120
QY 121 -YTFGQGTKEIK 132
   ||:||||:|
Db 121 plftfgagtkleik 133

```

## RESULT 8

R59509 standard; Protein; 133 AA.

AC R59509;

DT 31-DEC-1994 (first entry)

DE Sequence of the light chain variable region of the mouse NA-8

DE antibody, including the signal sequence and mature chain.

XX Antibody NA-8; human CD18; complementarity determining region; CDR;

XX Mus musculus.

XX Key Location/Qualifiers

XX Protein 21..133

XX /label= Mature light chain

XX WO9412214-A.

XX 09-JUN-1994.

XX 30-NOV-1993; 93WO-US11611.

XX 01-DEC-1992; 92US-0983949.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Co MS, Landolfi NF;

XX WPI; 1994-199973/24.

XX N-PSDB; Q66845.

XX New humanised antibodies specific for CD18 - derived from new

XX murine antibody NA-8, prevent binding of neutrophils to

XX endothelial cells, useful for treating inflammation

XX Disclosure; Fig 1A; 50pp; English.

XX The mouse antibody NA-8 binds to human CD18. cDNAs for the heavy

XX chain and light chain variable domain genes of NA-8 were cloned

XX using anchored PCR. The cDNA variable domain sequences and the

XX deduced AA sequences are shown in Q66845/R59509 and Q66846/R59510.

XX Sequence 133 AA;

```

Query Match      82.2%; Score 559.5; DB 15; Length 133;
Best Local Similarity 80.5%; Pred. No. 1.5e-37;
Matches 107; Conservative 15; Mismatches 10; Indels 1; Gaps 1;

```

```

QY 1 MDSQAOVLILLVSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 wygqkpgpspklllywasaresyvpdrfsgsggtftltitssvgaedvayycqyysy 120
QY 121 -YTFGQGTKEIK 132
   |||:||||:|
Db 121 plftfgagtkleik 133

```

```

RESULT 9
P80894
ID P80894 standard; protein: 133 AA.
XX
AC P80894;
XX
DT 03-DEC-1990 (first entry)
XX
DE V region of L chain of anti-P.aeruginosa exotoxin Ab #1.
XX
KW Pseudomonas aeruginosa; anti-exotoxin antibody; L chain; V region;
XX ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label=signal peptide
FT Region 21..133
FT /label=V region of L chain
XX
PN EP270077-A.
XX
PD 08-JUN-1988.
XX
PE 01-DEC-1987; 87EP-0117760.
XX
PR 03-DEC-1986; 86JP-0288340.
PR 26-NOV-1987; 87JP-0298513.
XX
PA (SUMO) SUMITOMO CHEM IND KK.
XX
PI Nakatani T, Nomura N, Horigome K, Noguchi H;
XX
DR WPI: 1988-156310/23.
DR N-PSDB; N80499.
XX
PT New gene encoding for antibody to Pseudomonas aeruginosa exotoxin -
PT plus recombinant vectors and host cells, useful for treating
PT infections.
XX
PS Claim 4; Page 25; 39pp; English.
XX
CC Sequence is variable region of light chain of anti-exotoxin
CC antibody with signal sequence. N80498 encodes the same sequence
CC except that its signal peptide-encoding sequence contains an
CC intron.
CC See also N80495-N80496, N80498 and N80941-2.
XX
SQ Sequence 133 AA;

Query Match 81.9%; Score 557.5; DB 9; Length 133;
Best Local Similarity 84.6%; Pred. NO. 2,1e-37;
Matches 110; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

OY 4 QAOVILLLLWVSGTCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENTLAWTQ 63
DB 4 qtvvftislllwsgsgydlvmtdpsdlsavslgeratlnckssgsvlysnknkylawyq 63
OY 64 QKPGPPKILTYWASTRSGVDPDRSGSGGSDTPTLTSSLQAEADVAVYYCTQSYNL-VT 122
DB 64 qkpqppkillywastresgydpdrtsqsgsdftcltsslaqadvavyycqgysstprt 123
OY 123 FGQGTKEVEIK 132
DB 124 fgggtkveik 133

RESULT 10
W06206
ID W06206 standard; Protein: 134 AA.

```

```

XX AC W06206;
XX
DT 17-FEB-1997 (first entry)
XX
DE Xenograft antibody HAR-1 kappa light chain variable region.
XX
KW Xenograft rejection; xenotransplantation; organ transplant;
KW animal model; hamster; monoclonal antibody; HAR-1.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Region 1..20
FT /label= Leader
FT Region 21..43
FT /label= FR-1
FT /note= "Framework region 1"
FT Region 44..60
FT /label= CDR-1
FT /note= "complementarity determining region 1"
FT Region 61..75
FT /label= FR-2
FT /note= "Framework region 2"
FT Region 76..82
FT /label= CDR-2
FT /note= "complementarity determining region 2"
FT Region 83..114
FT /label= FR-3
FT /note= "Framework region 3"
FT Region 115..122
FT /label= CDR-3
FT /note= "complementarity determining region 3"
FT Region 123..134
FT /label= FR-4
FT /note= "Framework region 4"
XX
PN W0636358-A1.
XX
PD 21-NOV-1996.
XX
PE 14-MAY-1996; 96WO-US06804.
XX
PR 15-MAY-1995; 95US-0440621.
XX
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI Cramer DV, Makowka L, Wu G;
XX
DR WPI: 1997-011852/01
DR N-PSDB; T43415.
XX
PT Inhibiting xenograft rejection by modifying antigen expression of
PT the graft - prevents binding of anti-donor antibody and prolongs
PT graft survival
XX
PS Claim 11; Page 99; 135pp; English.
XX
CC A polypeptide (W06206) comprises the kappa light chain variable
CC region of the LEW rat anti-hamster xenograft monoclonal antibody
CC HAR-1. It is encoded by a cDNA clone (T43415) obtd. from a HAR-1
CC hybridoma light chain cDNA library; the hybridoma was produced by
CC fusing spleen cells of a LEW rat that had received a hamster heart
CC transplant, with rat myeloma cells. Recombinant fragments, e.g.
CC Fab'(1/2 and Fab', of the antibody block binding of preformed
CC anti-donor xenograft antibodies in a recipient animal serum to
CC antigen expressed by endothelial cells of the xenograft, i.e. they
CC inhibit antibody-mediated rejection, thereby prolonging the
CC survival of the hamster xenograft in the recipient.
XX
SQ Sequence 134 AA;

```

Query Match	81.8%	Score 557	DB 18	Length 134
Best Local Similarity	76.8%	Pred. No. 2.3e-37		
Matches 104	Conservative 14	Mismatches 14	Indels 0	Gaps 0
OY	1	MDSQAQVILLILWVSGTGDIVLQSPDSLAVSLGERATISCKSSQSLNSTRRENTYLA	60	
DB	1	mesqgvlmslllwsygtcgdlvmqtpssqvasagekvtmcskssqsllynenknyla	60	
OY	61	WTQKPGCPKLLIYASTRESGVDPDRSGSGSGIDFTLITISLQAEVAVYCTQSYNL	120	
DB	61	wyrgkpgspsklllywastresgvpdrfllgsgsgldflltllssvgaedlavyycqyyyl	120	
OY	121	YFEGGTKEIK 132		
DB	121	ylfagqtkleik 132		
RESULT 11				
ID	Y24374	standard; Protein; 141 AA.		
XX	Y24374;			
XX	17-SEP-1999	(first entry)		
DE	Human monoclonal antibody against CTGF SEQ ID NO:16.			
XX	Human monoclonal antibody; connective tissue growth factor; CTGF;			
KW	cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;			
KW	skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;			
XX	rheumatic vascular inflammation.			
OS	Homo sapiens.			
XX	MO993878-A1.			
PN	08-JUL-1999.			
PD	16-DEC-1998;	98WO-JP05697.		
XX	15-DEC-1998;	98JP-0356183.		
PR	25-DEC-1997;	97JP-0367699.		
XX	(NIBS ) JAPAN TOBACCO INC.			
PA	Sakamoto S, Takigawa M, Tamatani T, Tezuka K;			
XX	WPI. 1999-430232/36.			
DR	N-PSDB; X90025.			
XX	New monoclonal antibody reactive with connective tissue growth			
PT	factor useful in the treatment of cell proliferation disorders			
XX	Claim 18; Page 191-192; 212pp; Japanese.			
PS	X90020 to X90029 encode monoclonal antibodies which react with human			
XX	connective tissue growth factor (CTGF). Y24369 to Y24378 represent			
CC	these monoclonal antibodies. The antibodies are useful in the diagnosis,			
CC	prevention and treatment of cell proliferation disorders in which CTGF			
CC	is implicated, including fibrosis of lung, kidney, liver and other			
CC	tissues; liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid			
CC	arthritis; rheumatic vascular inflammation; hepatitis; and cancer.			
XX	Sequence 141 AA;			
Query Match	81.5%	Score 555;	DB 20;	Length 141;
Best Local Similarity	82.4%;	Pred. No. 3.5e-37;		
Matches 108;	Conservative 9;	Mismatches 12;	Indels 2;	Gaps 1;
OY	4	QAQVILLILWVSGTGDIVLQSPDSLAVSLGERATISCKSSQSLNSTRRENTYLA	63	
DB	4	qgqvllllllwsgygdvlvmqtpssqslavsgatlnckssqsllysnmknylawyq	63	

```

Oy      64  OKPGPPKLLIYMASTRSGVDPFRSGSGSGDFLTLTSSLOAEVAVAYCYQSYNLT--Y 121
Db      64  qKpggpKkLLIlywastrsgvdpfrtsgsgsgdfcltltlsslgadavayycqgqystppw 123
Oy      122  TFGGCTKWEIK 132
Db      124  tfggctkweik 134

RESULT  12
ID      B03714
AC      B03714 standard; protein; 135 AA.
XX
XX      B03714;
XX
XX      04-OCT-2000 (first entry)
DT
DE      Immunoglobulin kappa2 amino acid sequence fragment.
KW
KW      Aortic aneurysm-associated antigen protein; AAP; microfibrillar protein;
KW      abdominal aortic aneurysm disease; treatment; detect; tolerance;
KW      Immunoglobulin kappa; IgK.
XX
XX      Unidentified.
OS
XX      US6048704-A.
XX      11-APR-2000.
PD
XX      07-MAR-1997; 97US-0812586.
PF
XX      07-MAR-1996; 96US-0012976.
PR
XX      (UYCO ) UNIV COLUMBIA NEW YORK.
PA
XX      Tilson MD:
PI
XX      WPI: 2000-316895/27.
DR
XX
XX      Isolated microfibrillar protein for alleviating abdominal aortic
XX      aneurysm disease is purified from human aortic tissue and binds
XX      immunoreactively with immunoglobulin -
XX
XX      Example 3; Column 30; 70pp; English.
XX
XX      The present invention relates to an isolated microfibrillar protein of
XX      approximately 40KD. The protein is isolated from human aortic tissue and
XX      binds immunoreactively with immunoglobulin purified from human abdominal
XX      aortic aneurysm (AAA) tissue. The protein is referred to as aortic
XX      aneurysm-associated antigenic protein (AAP). The protein is capable of
XX      forming a disulphide bonded dimer. The protein is immunoreactive with
XX      human kappa immunoglobulin. Also included in the invention are
XX      recombinantly produced human AAA proteins. AAP shows regions of homology
XX      with the bovine microfibril associated glycoprotein MFAP-4 and also with
XX      fibrinogen and vitronectin. The isolated microfibrillar protein is useful
XX      for alleviating abdominal aortic aneurysm (AAA) disease and detecting the
XX      presence of AAA-associated immunoglobulin bound to the human aortic
XX      tissue. Antibodies directed against AAP can be used to detect AAA
XX      disease. The recombinant protein can be used to induce tolerance to
XX      antigenic AAA protein in the subject e.g. human. This sequence represents
XX      an immunoglobulin kappa2 amino acid sequence. The sequence shares
XX      homology with the AAP of the invention, it was used to identify and
XX      characterise AAP.
XX
XX      Sequence 135 AA:
SQ

Query Match      81.3%; Score 553.5; DB 21; Length 135;
Best Local Similarity 84.6%; Pred. No. 4,5e-37;
Matches 110; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

```

```

Db      4 qtqfjlllwlsgaydvlwmtgspdsldvslgeratlnckssgsllyssnnknylawyq 63
Qy      64 QKPCQPKLLIYMASTRSGVDPDRFSGSGTDPFTLTITSSLAQADVAVYCTOSYNL-yr 122
        64 qkpgqppklllywastresgyvdrfsgsgtdftltlsslaqadvaavyccqyyslcpmm 123
Qy      123 FGQCTKVEIK 132
        124 fggqtkveik 133
Db      124 fggqtkveik 133

RESULT  13
R28809  ID R28809 standard: Protein: 241 AA.
AC      R28809:
XX
XX
DT      02-APR-1993 (first entry)
XX
XX      Vector PMDR1007.
DE
XX      Plasmid: PMDR1006: psAB132; vector: PMDR1007: PMDR985; AatII: EcoRV;
KM      PMDR986: BglIII: PMDR1003: JA221(Iq); E. coli: ampicillin resistance;
KM      NotI: dephosphorylate; calf: alkaline phosphatase; low temperature;
KM      melting agarose; immunoglobulin: kappa chain; signal peptide; LC;
KM      humanised: 5A8; light chain: variable region; LV: genomic; constant
KM      antibody; homolog: CD4; gp120; cell surface; glycoprotein; CD4+;
KM      lymphocyte; helper; inducer; HIV; syncytia; formation.
XX
XX      Synthetic.
OS
XX      Key
FH      Peptide
FT      1..22
FT      /note="Immunoglobulin kappa chain signal peptide"
FT      23..134
FT      /note="Humanised 5A8 LV"
FT      135..241
FT      Region
FT      /note="Human kappa chain LC"
XX
XX      WO9209305-A.
XX
XX      11-JUN-1992.
XX
XX      27-NOV-1991: 91WO-US08843.
XX
XX      27-NOV-1990: 90US-0618542.
XX
XX      (BIOI ) BIOGEN INC.
XX
XX      Burklly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
XX
XX      WPI: 1992-398399/48.
XX
XX      N-PsDB: Q30920.
XX
XX      New anti-CD4 antibody homologues - which bind CD4, do not block
XX      binding of HIV gp120 to CD4 but block HIV-induced syncytia
XX      formation between CD4+ cells
XX
XX      Disclosure: Page 166-7; 205pp; English.
XX
XX      The sequence given is encoded by the insert of the vector PMDR1007.
XX      PMDR1006 (see Q30919) and psAB132 (see Q30906) were used in the
XX      construction of this vector. Three fragments were ligated together
XX      to generate PMDR1006: a 572 bp fragment of PMDR985 (see Q30913), a
XX      342bp AatII/EcoRV fragment of PMDR986 (see Q30918) and a 326 bp
XX      EcoRV/BglIII fragment of PMDR1003 (see Q30900). The ligation mixture
XX      was used to transform E. coli JA221(Iq) to ampicillin resistance.
XX      PMDR1006 was cleaved with NotI and the 1693 bp fragment isolated was
XX      ligated into NotI linearised psAB132 which had been dephosphorylated
XX      by calf alkaline phosphatase. This generates the plasmid PMDR1007.
XX      The dephosphorylated mixture was fractionated through low temperature
XX      melting agarose and used to transform E. coli JA221(Iq) to ampicillin

```

```

CC      resistance. The PMDR1007 insert comprises DNA encoding, in a 5' to 3'
CC      order, the immunoglobulin kappa chain signal peptide, amino acid (AA)
CC      1-AA112 of the humanised 5A8 light chain variable region (LV) followed
CC      by genomic DNA encoding AA108-AA214 of the human kappa light chain,
CC      ie. the light chain constant region (LC). This polypeptide is an
CC      antibody homolog which was shown to bind to CD4 but did not block the
CC      binding of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4+
CC      lymphocytes (helper/inducer cells). The homolog blocked HIV-induced
CC      syncytia formation. This homolog can be used in the detection,
CC      prophylaxis and treatment of diseases caused by infective agents whose
CC      primary targets are CD4+ cells.
XX
XX      Sequence 241 AA:
SQ
XX
XX      Query Match
XX      Best Local Similarity 183.6%; Score 548; DB 13; Length 241;
XX      Matches 107; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
Qy      5 AOVLLILLVWSTCGDIVLTOSPDLSAVSLGERATVRSCKSSQSLNSTRBNYLAWYQ 64
        7 aqlllglllllwlpgargdvlwmtgspdsldvslgeratlnckssgsllystngknylawyq 66
Qy      65 KPCQPKLLIYMASTRSGVDPDRFSGSGTDPFTLTITSSLAQADVAVYCTOSYNLITFG 124
        67 kpgqppklllywastresgyvdrfsgsgtdftltlsslaqadvaavyccqyysyrtfg 126
Qy      125 OGKTKVEIK 132
        127 rgtkveik 134
Db      127 rgtkveik 134

RESULT  14
Y50161  ID Y50161 standard: Protein: 240 AA.
XX
XX      Y50161:
XX
XX      31-JAN-2000 (first entry)
XX
XX      Human reshaped F19 antibody light chain (version a).
DE
XX
XX      Antibody: monoclonal; F19; fibrinogen activation protein alpha; FAP;
XX      humanisation; complementarity determining region; CDR: CDR grafting;
XX      reshaped; reactive stroma; fibroblast; epithelial cancer;
XX      diagnosed; immune response; framework sequence; constant region;
XX      variable region; productivity; treatment; cancer; colorectal; lung;
XX      breast; head; neck; ovarian; lung; bladder; pancreatic; metastasis;
XX      detection; wound healing; skin inflammation; tumour; immunogenicity;
XX      chimeric; light chain.
XX
XX      Chimeric - Mus sp.
OS
XX      Chimeric - Homo sapiens.
XX
XX      Key
FH      Peptide
FT      1..20
FT      /note="Leader peptide"
FT      21..240
FT      /note="Mature human reshaped F19 light chain"
FT      21..140
FT      /note="Mature reshaped human F19 light chain variable
FT      region"
FT      44..60
FT      /note="Complementarity determining region (CDR) 1"
FT      76..82
FT      /note="CDR 2"
FT      115..123
FT      /note="CDR 3"
FT      141..240
FT      /note="Human kappa light chain constant region"
XX
XX      EP953639-A1.
XX

```

PD 03-NOV-1999.  
 XX  
 PF 30-APR-1998; 98EP-0107925.  
 XX  
 PR 30-APR-1998; 98EP-0107925.  
 XX  
 PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 XX  
 PI Park JF, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;  
 PI Reticig WJ;  
 XX  
 DR WPI: 1999-621833/54.  
 DR N-PSDB: 232784.  
 XX  
 PT New antibody protein, useful for treating cancer and for imaging  
 PT presence of activated stromal fibroblasts in healing wound or inflamed  
 PT skin -  
 XX  
 PS Example 3; Fig 30; 143pp: English.

CC This sequence represents the light chain (version a) of a reshaped human  
 CC F19 antibody. F19 (ATCC Accession number HB 8269) is a murine monoclonal  
 CC antibody against fibroblast activation protein alpha (FAP). FAP is a cell  
 CC surface molecule of reactive stromal fibroblasts, and its induction  
 CC is a highly consistent molecular trait of the reactive stroma of many  
 CC types of epithelial cancer. Although F19 may be useful in vitro, e.g.,  
 CC for diagnosis, its applications for in vivo use in humans are problematic  
 CC as it elicits a human anti-mouse response which reduces the efficacy of  
 CC the antibody in patients and impairs continued administration. The  
 CC novel human reshaped F19 was humanised by grafting the murine  
 CC complementarity determining regions (CDRs) of F19 onto human variable  
 CC region framework sequences, and then joining these "reshaped human"  
 CC variable regions to human constant regions. These modifications  
 CC also result in the improved producibility in eukaryotic cell culture  
 CC systems as compared to a chimeric antibody having the entire variable  
 CC regions of F19 joined to human constant regions. The human reshaped F19  
 CC antibody has low immunogenicity for humans and is useful for treating  
 CC cancers e.g., colorectal cancers, non-small cell lung cancers, breast  
 CC cancers, head and neck cancers, ovarian cancers, lung cancers, bladder  
 CC cancers, pancreatic cancers and metastatic cancers. It is also useful for  
 CC the detection of activated stromal fibroblasts in a healing wound,  
 CC inflamed skin or a tumour in a human patient.

XX Sequence 240 AA:

Query Match 80.4%; Score 547.5; DB 20; Length 240;  
 Best Local Similarity 82.1%; Pred. No. 2.3e-36;  
 Matches 110; Conservative 10; Mismatches 11; Indels 3; Gaps 2;

QY 1 MDSQAQVLLILLMWSTGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60  
 DB 1 mecdtlllwlllwpqsgdlymltspsdlsavslgeratlnssqsllysrnqkyla 60  
 QY 61 WYQOKPGQPKLLIYMASTRESGVPDRFSSGSGTDTLTITSSLOADVAIVYCTQ--SY 118  
 DB 61 wygqkpgqpklllywastresgyvdrfssgsgtdltltltslsgaedavvyvcqgyfsy 120

QY 119 NLTFGQGTKEIK 132  
 DB 121 pl-tfgqgtkveik 133

RESULT 15  
 R85909 standard; Protein; 133 AA.

AC R85909;

DT 02-JUL-1996 (first entry)

XX Monoclonal antibody, CB-Hep.1, light chain variable domain.

KW HBV; hepatitis B virus surface antigen; monoclonal; antibody;  
 KW CB-Hep.1; immunopurification; detection; hybridoma; recombinant;  
 KW Fv; variable; VH; HBsAg.

XX Mus sp.

XX Key Location/Qualifiers  
 FH Peptide 1..20  
 FT /label= sig\_peptide  
 FT 21..133  
 FT Protein /label= mat\_protein  
 FT 21..43  
 FT Domain /label= FR1  
 FT 44..60  
 FT Domain /label= CDR1  
 FT 61..75  
 FT Domain /label= FR2  
 FT 76..82  
 FT Domain /label= CDR2  
 FT 83..114  
 FT Domain /label= FR3  
 FT 115..123  
 FT Domain /label= CDR3  
 FT 124..133  
 FT Domain /label= FR4

PN EP686696-A1.

PD 13-DEC-1995.

PF 09-JUN-1995; 95EP-0201535.

PR 09-JUN-1994; 94CU-0000073.

PA (ING-) CENT ING GENETICA & BIOTECNOLOGIA.  
 PA (KAMB/) KAMBEEL R W.

PI Ayala Avila MA, Canaan-Haden Frias LM, del Carmen Dominguez Horta MC;  
 PI Fernandez de Cossio Dorta-Dugue ME, Gavilondo Cowley JVG;  
 DR WPI: 1996-021914/03.  
 DR N-PSDB: Q74067.

PT New recombinant single chain Fv antibody fragment - useful for  
 PT immuno-purificn. and detection of HBsAg

PS Claim 1; Page 19; 23pp: English.

CC R85908 and R85909 are the heavy and light chain variable domains of  
 CC the murine hybridoma-derived monoclonal antibody CB-Hep.1 Fv region.  
 CC The heavy and light chain regions are used to produce a recombinant  
 CC antibody fragment having specificity for the hepatitis B virus  
 CC surface antigen (HBsAg). The recombinant antibody may be used for  
 CC immunopurification of HBsAg, in immunoassays for the detection of  
 CC HBsAg and for insolubilisation of heterologous fusion proteins  
 CC expressed in E. coli aiding their purification.

XX Sequence 133 AA:

Query Match 80.0%; Score 544.5; DB 17; Length 133;  
 Best Local Similarity 78.2%; Pred. No. 2.3e-36;  
 Matches 104; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

QY 1 MDSQAQVLLILLMWSTGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60  
 DB 1.mdsqayvlmllllwsqsgdlymgspslavsgekvalsckssqslly]nmhkyla 60

QY 61 WYQOKPGQPKLLIYMASTRESGVPDRFSSGSGTDTLTITSSLOADVAIVYCTQSYNL 120  
 DB 61 wfqgkpgqpklllywastresgyvdrfssgsgtdltltlssvkaedlavvyvcqgyyny 120

QY 121 -YTFGQGTKEIK 132

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Db 121 pytf99g9tklelk 133

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Job time: 69 sec